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OM nucleic - nucleic search, using sw model Run on:

May 9, 2004, 03:49:53; Search time 5075:84 Seconds (without alignments) 10554.310 Million cell updates/sec

1 atgagtgaaagtgacgaaac.....aaaacatcagtgatttctcga 1236 US-09-831-804-1_COPY_720_1955 Title: Perfect score: Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

6940544 3470272 seqs, 21671516995 residues Total number of hits satisfying chosen parameters: Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

GenEmbl:*

1: gb_ba:*

2: gb_htg:*

4: gb_ow:*

5: gb_ov:*

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16: em_fun:*

17: em_ov:*

18: em_ni:*

19: em_ov:*

10: em_htg_nn:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Descriptio	74350 BD274350 Cand	74349 BDZ/4349 C	25 WOODE WOODE STATE OF THE STA	M80611 Sc	577 U25841 Sa	P026A M33924 S	06ING AL40051	38126 AC138126 F	73544 AC073544 H)42 AX714042	988 AKU56088	ACOSA	169 AC130403	D20831 HO	AC008739	AC011494	1 AR27049	'6 U35376 Hu	.32 BX000432 Mc	Х78932 Н. ва	9 AC092329 Hor	13 AC024483 Hor	7 AC105677 Ra	B C C C	AC420174	AC016628 Ho	AC012431 Ho	M55422 Human	G28705 SWS	59 G18281 h	3620 AC010620	AC141066	3210 ACU73210	AY044432 HOMO	3253 AA / 48253 Seq	AK093669 HOM	BX647875	BC036439 HOMO	AX747097 Seq	AK091618 Hom	40594 BC040
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ALIGNMENTS

BD274350
Candida albicans tfIIIAgene (CatfIIIA) and the coded CATFIIIA protein.
BD274350
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BD274350.1 GI:33084118
Candida albicans
Candida albicans
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; mitosporic Saccharomycetales; Candida.
I (bases 1 to 1239)
Pallier.F.B., Camier, S. and Sentenac, A. Candida albicans tfIIIAgene (CatfIIIA) and the coded CATFIIIA ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT 1 BD274350 LOCUS DEFINITION

REFERENCE AUTHORS TITLE

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Saccharomycetales, mitosporic Saccharomycetales, Candida.
                                                             781 TTAAAGGAAACTGAAGTGAAAAATTAGAGAACCTATTAGATCAAGGATCGAAATTAAAT
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OS Candida albicans
PN JP 2002531068-A/2
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PN JP 2002531068-A/2
PN 24-SEP-2002
PF 09-NOV-1998 FR 98/14147
PI FLORENCE BORDON PALLIER, SYLVIE CAMIER, ANDRE SENTENAC PC C12M15/09, C12N15/09, A61K39/00, A61K45/00, A61R31/10, C07K14/40, PC C07K16/14, C12N1/19, C12N1/21, C12P21/02, C12Q1/02, G01N33/56, G01N33/56
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  Patent: JP 2002531068-A 2 24-SEP-2002;
AVENTIS PHARMA SA
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  /organism="Candida albicans"
  /mol_type="genomic DNA"
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                                 GATAGTCTAGATGAAAAAAAGAAGTGATGTTAGATCAGACTCAATGTCAAAGGATCA
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Roemer,T., Jiang,B., Boone,C., Bussey,H. and Ohlsen,K.L.
Gene disruption methodologies for drug target discovery
Patent: WO 02053728-A 6493 11-JUL-2002;
Elitra Pharmaceuticals, Inc. (US)
Location/Qualifiers
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99.7%; Score 1232.8; DB 6
Best Local Similarity 99.8%; Pred. No. 1.4e-189;
Matches 1234; Conservative 0; Mismatches 2;
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Sequence 6493 from Patent WO02053728.
AX489193 GI:22323205
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DNA.

Original source text: Saccharomyces cerevisiae (strain S288C)
Location/Qualifiers
1. .1560
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/mol_type="genomic DNA"
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source

ORIGIN

JOURNAL MEDLINE PUBMED COMMENT FEATURES Gaps 9;

Indels

Length 1560;

1 (bases 1 to 1560)
90chik, N.A. and Young, R.A.
Genes encoding transcription factor IIIA and the RNA polymerase common subunit RPB6 are divergently transcribed in Saccharomyces cerevisiae

Proc. Natl. Acad. Sci. U.S.A. 89 (9), 3999-4003 (1992) 92237295 1570325 Original source text: Saccharomyces cerevisiae (strain

RNA polymerase; transcription factor IIIA.
Saccharomyces cerevisiae (baker's yeast)
Saccharomyces cerevisiae
Saccharomyces Pungi; Ascomycota; Saccharomyceties; Saccharomycetales;

SOURCE ORGANISM

KEYWORDS

REFERENCE AUTHORS TITLE

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Score 217.4; DB 8;
Pred. No. 9.9e-26;
0; Mismatches 271;
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1560 bp DNA linear PLN 27-APR-1993 Saccharomyces cerevisiae transcription factor IIIA and RNA polymerase subunit RPB6 genes. M90638

RESULT 4 YSCNOFEAT LOCUS DEFINITION

ACCESSION VERSION

723 481 963

655

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Controlled Saccharomyceters, saccharomycotina, Saccharomycetes, Bukaryotta, Pungi; Ascomycota, Saccharomycotina, Saccharomycetes, Saccharomyceteles, Saccharomyces, Saccharomyces, Saccharomyce, Du, Z., Satellon, A., Talton, L., Gattung, S., Greo, T., Kirsten, J., Kirsten, D., Ohnston, L., Langston, Y., Latrellle, P., Le, T., Nardis, E., Ohnston, L., Tanch, A., Trevaskis, E., Vignati, D., Wilcox, L., Wohldman, P., Vaudin, W., Wilson, R. and Waterston, R. The sequence of a portion of the right arm of Saccharomyces cerevisiae chromosome XVI

1. Unpublished (1995)
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This sequence includes nucleotides 1-37497 of cosmid 9677.
cosmid on the left is 9705.
Location/Qualifiers
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/organism="Saccharomyces cerevisiae"
/mol type="genomic DNA"
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Department of Genetics, Washing
St. Louis, NO 63110, USA
e-mail: mj@sequencer.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence of S. cerevisiae cosmid 9677 Unpublished (1995)
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Submitted (27-APR-1995) Robert Waterston
Submitted by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae (baker's yeast)
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RPRYPRODYDGCODKAPTRESILTEHOLSVHQGLARAPGODGCAKSFVKRAHLERLLYTH
SDTKPPGCSYGKGVTTRQQLKRHEVTHTKSFICPEBGCNLRPYKHPQLKSHLEKHLYTH
HKLTCPHCNKGSPORPYRLRNHISKHPOPEVERNPYQCTFAGCCKEFRINGQLGSHIKND
HPKLKCPICSKPCVGSNGLQMEMIIHDDSLYTKNWKHICDDMSFSRKHDLLTHYGSI
HTEBDIPLEBLKKISDTQQLVQDHQVQGLGNSKFSNEQDEEKISNRLRKRRKLTENNNV
BFLQNRVDLERKLESGSBNGLNLLLNTVGRKYRCFYRNCSRTFKTKEKYKTENNNV
BLYQKERENKTLVDQNHKEPFIIQKETGSAGDK"
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Saccharomyces cerevisiae transcription factor IIIA (TFIIIA) gene,
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The deduced sequence of the transcription factor TFIIIA from
Saccharomyces cerevisiae reveals extensive divergence from Xenopus
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transcription factor IIIA; zinc-finger protein; zinc-finger
transcription factor.
Saccharomyces cerevisiae (baker's yeast)
Saccharomyces cerevisiae
Eukaryota; Pungi; Ascomycota; Saccharomycotina; Saccharomycets;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.

1 (bases 1 to 1739)
Archambault, J., Milne, C.A., Schappert, K.T., Baum, B., Friesen, J.D.
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/gene="TFIIIA"
/note="zinc finger containing protein"
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/product="transcription factor IIIA"
/protein_id="AAB08014.1"
/db_xref="GI:172903"
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J. Biol. Chem. 267 (5), 3282-3288 (1992)
92147684
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/strain="W303-1A"
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14493. .15410
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5297. .9595
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5297. .9595
/ gene="SK13"
5297. .9595
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Matches 340;
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complement (16937...19570)
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                                                                                                                                                                                                                                                                                                                                                                                  ATTGTGATAAAGCATTTTTCAGAAAATCACATTTGGAAACACATATTGTATCACATTCCG
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                                                                                                                              Complement(16937. 19570)
Gene="P96771.13"
//note="Rimilar to S. cerevisiae hypothetical protein
HRD799 (PIR accession number S45161) and S. pombe
                                                                                                                                                                                                                                    ω
..
                                                                                                                                                                                                        Length 37497;
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                                                                                                                                                                                                       Score 217.4; DB 8;
Pred. No. 4.7e-26;
0; Mismatches 271;
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                                                                                                                                                                                                        Query Match
Best Local Similarity
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YSCRP026A 2133 bp DNA linear PLN 27-APR-1993 S.cerevisiae RNA polymerase II sixth subunit (RP026) gene, complete cds.

M33924

ACCESSION

YSCRP026A/c LOCUS DEFINITION

RESULT

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MNAPVFVDLEGETDPLKIAMKELAEKKIPLVIRRYLPDGSFEDWSVEELIVDL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Draft entry and computer-readable sequence for [Unpublished (1990)] kindly submitted by J.D. Friesen, 01-MAY-1990.

Dy J.D. Friesen, 01-MAY-1990.

SS University Avenue Toronto, CAMADA MSG 1X8

Toronto, Ontario, CAMADA MSG 1X8

e-mail: jim@sickkids.toronto.edu.
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M33924.1 GI:172452
RNA polymerase II; C-myc proto-oncogene; transmembrane protein; tyrosine kinase.
Saccharomyces cerevisiae (baker's yeast)
Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomycetes;
I (bases 1 to 2133)
Archambault, J., Schappert, K.T. and Friesen, J.D.
A suppressor of an RNA polymerase II mutation of Saccharomyces
Cerevisiae encodes a subunit common to RNA polymerases I, II, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              436 ccascaacrisasccsacscsascraacscaraccaaarcrircarristrcasscsasscs 377
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Original source text: S.cerevisiae single-copy plasmid DNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic DNA"
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/mol1026. .1045,1122. .1569)
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/note="RNA polymerase II sixth subunit (RP026)</pre>
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/note="RP026 intron A"
/note="RNA polymerase II sixth subunit
/note="RNA polymerase II sixth subunit
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91061718
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/organism="Saccharomyces
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ilarity 61.4%;
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AC138126 169063 bp DNA linear PRI 17-DEC-2002
Homo_sapiens chromosome 19 clone RPl1-274A19, complete sequence.
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1 (bases 1 to 169063)
DOE Joint Genome Institute and Stanford Human Genome Center.
/db_xref="taxon:4931"
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/note="end :T7"
<2. >796
/note="similar to Saccharomyces cerevisiae ORF YPR186c
PZF1 ; TFIIIA (transcription initiation factor) |"
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DOB Joint Genome Institute and Stanford Human Genome Center
Direct Submission
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                                                                                                                                                                                                                                        Length 797;
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                                                                                                                                                                                                                                          Score 193; DB 11; Length 7
Pred. No. 1e-21;
1; Mismatches 231; Indels
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AC138126.1 GI:27151357
                                                                                                                                                                                                                                          Match 15.6%;
Local Similarity 59.3%;
les 347; Conservative
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Homo sapiens
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L Submitted (07-28P-2000) Genoscope - Centre National de Sequencage,

2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail:
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail:
3 seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)

This 57S is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces survazzii, Zygosaccharomyces rouxii, Saccharomyces fulyverii, Kluyveromyces pararianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia libolyfica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequence of the other extremity of this sequence and for the sequence of the other extremity of this insert.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  006 NOV-2001 ONA linear STS 30-NOV-2001 end of clone ASOAA022B07 of library ASOAA from strain CLIB 533 Saccharomyces bayanus, sequence tagged site.
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                                                                                                                                                                                                                                                  645 TATGTTAAGTCATGATGATTCTACCATGATCAAAATATGGACTTGTGATTATTGTGATGT 704
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Bon, E., Neuveglise, C., Casaregola, S., Artiguenave, F., Wincker, P., Aigle, M. and Durrens, P.

Genomic exploration of the hemiascomycetous yeasts: 5.

Saccharomyces bayanus var. uvarum
FEBS Lett. 487 (1), 37-41 (2000)
          TCACATTICTAAACAICACGAICCTGAGGIAGAAAAICCTIACCAAIGIACTITIGCIGG 197
                                                                                                                                                                                                 77
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Bolotin-Futuhara, M., Bon, E., Brottier, P., Casaregola, S.,
Bolotin-Futuhara, M., Bon, E., Brottier, P., Casaregola, S.,
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Saurin, W., Tekata, F., Toffano-Nicohe, C., Wesolowski-Louvel, M.,
Wincker, P. and Weissenbach, J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
FEBS Lett. 487 (1), 3-12 (2000)
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Direct Submission
Unpublished
2 (Dases 1 to 17299)
Dos Joint Genome Institute.

Submitted (22-UTW-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (Dases 1 to 17729)
DOE Joint Genome Institute and Stanford Human Genome Center.
           l (bases 1 to 177299)
30E Joint Genome Institute and Stanford Human Genome Center.
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Submitted (17-DEC-2002) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA Drive, Walnut Creek, CA 94598, USA Drive, Walnut Creek, CA 94598, USA Waw.igi.doe.gov
Finishing Completed at Stanford Human Genome Center www.spic.doe.gov
Finishing Completed at Stanford Human Genome Center www.spic.dee.gov
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Direct Submission
Submitted (19-UNA-2002) DOE Joint Genome Institute, 2800 Mitchell
Submitted (19-UNA-2002) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Jun 19, 2002 this sequence version replaced gi:13699752.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
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                                                                                                                                                                                                                    www-shgc.stanford.edu
Quality:Phrap Quality >=40 99.9% of Sequence;
Estimated Total Number of Errors is 0.2.
NOTE: BACTERIAL TRANSPOSONS excised at 14620 and 98099.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 101; DB 9; Length 177299;
Pred, No. 2e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches 280; Indels
                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="RP11-359H18"
                                                                                                                                                                                                                                                                                                                                          location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 50.8%;
Matches 298; Conservative
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Homo sapiens chromosome 19 clone

RESULT 10
AC073544/C
LOCUS
DEFINITION
ACCESSION
KEYWORDS
SOURCE

ORGANISM

AC073544.4 GI:21465367

Homo sapiens (human) Homo sapiens Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

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LOCUS
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                                                       RESULT 12
AK056088
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JOURNAL
REFERENCE
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TITLE
JOURNAL
                                                                                                                                                                                     ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                Isogai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S.,
Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R.,
Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and
                                                                                                                                   PAT 15-APR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1384 GAATGTGGCAAAGCTTTTAACCAGTCCTCAATCCTTACTACACATAAGAGAATTCATACT 1443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1558 GGCAAAGCCTTTAACCACTCCTCACACCTTGCTACACATAAGGTAATTCATACTGGAGAG 1617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1618 AAACCCTACCAATGTGAAGAATGTGGTAAAGCCTTTAACCAGTCCTCACACCTTACTAGA 1677
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1858 TATGCTGGTGAGAAATCTTAGAAATGTGAAGAATGTAACAAAACCTTTAAAAGTTGTCAC 1917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                187 GATAAAGCATTTTTCAGAAAATCACATTTGGAAACACATATTGTATCACATTCCGAAAAA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              367 TATAAACATCATTTAA---GACATCATATATTATCTGTTCATGAAAAACATTAACG 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  424 TGTAAACAATGTAATAAAGTTTTCACTCGACCTTCAAAATTAGCACAACATAAATTAAAA 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       484 CATCATGGTGGATCTCCTGCTTATCAATGTGATCATCCTGGTTGTTTTAAAATTTTCCAA 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 GAAAGTGACGAAACCAAATCGATATCATCTTTAATATCTTCTTCTTCATCACGTCCC 66
                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Full-Length cDNAs
Full-Length cDNAs
Patent: EP 1293569-A 726 19-MAR-2003;
Helix Research Institute (JP) ; Research Association for
Biotechnology (JP)
Location/Qualifiers
163206 ACTIGATIGIGCATAAGATAATICATACTAAAAAAAAAACCTACAAGT 163160
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                                                                                                                                   linear
                                                                                                                                DNA

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    /db_xref="taxon:9606"

                                                                                                                             2132 bp | 1
Sequence 726 from Patent EP1293569.
                                                                                                                                                                                                      AX714042.1 GI:29888970
                                                                                                                                                                                                                                                           sapiens (human)
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Best Local Similarity 50.6
Matches 297; Conservative
                                                                                                                                                                                                                                                                                       sapiens
                                                                                                                          AX714042
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                                                                                                                                                                                                                                                        Homo
                                                                        RESULT 11
AX714042
LOCUS
DEFINITION
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VERSION
KEYWORDS
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                                                                                                                                                                                                                                                                                 ORGANISM
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JOURNAL
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mRNA linear PRI 01-AUG-2002 clone NT2RI2000341, moderately
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Direct Submission

Submission

Submission

Genomics (24-OCT-2001) Takao is Genomics (Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-396)

NEDO human comba sequencing project supported by Ministry of Economy, Trade and Industry of Japan; CDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5- & 3-end one pass sequencing: RAB, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: RAB, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DKARNQSSTLTTHKI IHTREKLNEYKECGKARNQSSHLTRHKI IHTGEKPYKCEECGK
AFNQSSHLTRHKI IHTGEKPYKCEECGKARRQSSHLTTHKI IHTGEKPYKCEECGKARNOSSHLTRHKI IHTGEKPYKCEECGKARNOSSHLTBHKNI IHTGEKPYKCEECGKARNOSSHLTBHKNI IHTGEKPYKCEECGKARNOSSHLTBHKNI IHTGEKPYKCEECGKARNOSSHLTRKI IHTGEKPYTCEECGKARNOSSHLTBHKKI IHTGEKPYTCEECGKAFNSSHLATHKVI IHTGEKPYCEECGKAFNGSSHLTEHKKI IHTGEKPYCEECGKAFNGSSHLTRHKRI IHTGEKPYQCEKCGKAFNGSSHLTRHKKI IHTGEKPYQCEKCGKAFNGSSHLTGHKKI IHTGEKLYKPKRCNSDFENTSKFSK
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BCGKANOĞFNNLTHAKIIYTRDKLYKREEGSKAFRLSSHITTHTIIHTGENPYKREEG
                                                                                                                                                                                                                                                                                                                                                                                                                       Ninomiya,K., Wagatsuma,M., Kanda,K., Kondo,H., Yokoi,T.,
Kodaira,H., Furuya,T., Takahashi,M., Kikkawa,B., Omura,Y., Abe,K.,
Kamihara,K., Katsuta,N., Sato,K., Tanikawa,M., Yamazaki,M.,
Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S.,
Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S.,
Kamamoto,J., Isono,Y., Kawai-Hio,Y., Sato,H., Wahama,T.,
Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M.,
Kikuchi,H., Murakawa,K., Kanehori,K., Takahashi-Fujii,A.,
Nagahazi,K., Masuho,Y., Nagai,K. and Isogai,T., Sugano,S.,
Nashi, M., Nawakami,B., Suzuki,Y., Sugano,S.,
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                                                                                                                                                                                                                                                                                                              Eukaryoča, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates; Catarrhini, Hominidae; Homo.
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                                                                   AAUS6088.1 GI:16551397
oligo capping; fis (full insert sequence)
Homo sapiens
Eukarvet
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/note="unnamed protein product"
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AKOS6088 2132 bp
Homo sapiens cDNA FLJ31526 fis, clc
similar to ZINC FINGER PROTEIN 43.
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Best Local Similarity 50.6
Matches 297; Conservative
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48699 GAATGTGGCAAAGCTTTTAACCAGTCCTCAATCCTTACTACATAAAAAGAATTCATACT 48640
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48579 ACTGAACATAAGAAATTCATACTGGAGAAACCCTACACATGT-----GAAGAATGT 48526
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SEQUENCING IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TATAAACATCAATCTTTAA---GACATCATATTATTTTCTGTTCATGAAAAACATTAACG 423
Estimated Total Number of Errors is 0.1.

NOTE: This insert is not the entire sequence of the clone (entire sequence is 133.8kb). It is clipped at the overlap with AC008981. The number of seases overlapped is 27192.

In .138627
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DOB Joint Genome Institute and Stanford Human Genome Center. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18405 CATAAGAGAATTCATACTGGAGAAACCCTACCAATGTGAAAAATGTGGCAAAGCTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATCATGGTGGATCTCCTGCTTATCAATGTGATCATCCTGGTTGTTTTAAAATTTTCCAA
                                                                                                                                                                                                                                                                                                                                                                                                 7 GAAAGIGACGAAACCAAATCGATAICAICITIAAIAICTICTICTICTICAICACGICCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 AAAAAGTATATTTGCACATATGAAGGGTGTGATAAAGCCTATAATCGACCATCATTATTA
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Homo sapiens chromosome 19 clone RP11-189C24, PROGRESS ***, 5 ordered pieces.
                                                                                                                                         /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="texon:9606"
/chromosome="19"
/clone="RP11-20946"
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Homo sapiens chromosome 19 clone RP11-209J6, complete sequence.
ACO99500
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DOE Joint Genome Institute.

DOE Joint Genome Institute.

Submitted (12,00V-2001) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA (Dases I to 138627)

DOE Joint Genome Institute and Stanford Human Genome Center.

Direct Submitsed (29-MAY-2002) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94599, USA

On May 29, 2002 this sequence version replaced gi:16930916.

Draff Sequence Produced by DOE Joint Genome Institute
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( Chases 1 to 138627)

DOE Joint Genome Institute and Stanford Human Genome Center.

Direct Submission

Unpublished
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                                                                           1384 GAATGTGGGAAAGCTTTTAACCAGTCCTCAATCCTTACTACACATAAGAGAATTCATACT
                                                                                                                     AAAAAGTATATTTGCACATATGAAGGGTGTGATAAAGCCTATAATCGACCATCATTATTA
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                              GAAAGTGACGAAACCAAATCGATATCATCTTTAATATCTTCTTCTTCTTCATCACGTCCC
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hinshing Completed at Stanford Human Genome Center
www-shors stanford.edu
Quality: Phrap Quality >=40 100% of Sequence;
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E 2 (bases) to 2237)

E 2 (bases) to 2003) Takao Isogai, FLJ Project (HRI Team); 2-6-7

E mailigenomicsobri.co.jp, Tella 1438-52-3975, Fax:81-438-52-3966)

E mailigenomicsobri.co.jp, Tella 4.38-52-3975, Fax:81-438-52-3966)

EDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan, cDNA full insert sequencing: Research Association for Biotechnology (RAB); CDNA ilbrary construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center, National Institute of Technology and Byaluation; clone selection for full insert sequencing: RAB, annotation: HRI and RAB, annotation: HRI and RAB, annotation: HRI and RAB.
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Homo sapiens CDNA FLJ16502 fis, clone FBBRA2006664, moderately similar to Zinc finger protein 43.

AK122869 I GI:34528067
Oligo capping, fis (full insert sequence).

Homo sapiens (human)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                    49433 AAACCCTACCAATGTGAAGAATGTGGTAAAGCCTTTAACCAGTCCTCACACCTTACTAGA
                                                                                                                                                                                                                                         49373 CATAAGAGAATTCATACTGGAGAGAAACCCTACCAATGTGAAAAATGTGGCAAAGCTTTT
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                    247 AAACCATTCCATTGTTCAGTGTGTGTAAAGGGGTTAATTCTCGACAACACTTGAAAAGA
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AL Unpublished

CE 2 (bases 1 to 169500)

RS DOE Joint Genome Institute and Stanford Human Genome Center.

Direct Submission

NAL Drive, Walnut Creek, CA 94598, USA

T NOTE: This is a "working draft, sequence. It currently

* Consists of 5 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* TS997 138071: contig of f2175 bp in length

* 75997 138071: contig of f2175 bp in length

* 138072 13899: contig of 19728 bp in length

* 158000 157999: gap of unknown length

* 158000 166058: contig of 19728 bp in length

* 166059 166158: gap of unknown length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality coverage: 0 in Q20 bases; agarose-fp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Project Information
Center Project Name: 479013
Center clone name: RP11-189C24
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="texon:9606"
/chromosome="19"
/clone="RP11-189C24"
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                                                                                                                                                                                                                                                                                                           1712 TGAACATAAGAAATTCATACTGGAGAAACCCTACACATGT-----GAAGAATGTGG 1765
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1886 TAAGAATTCATACTGGAGAAACCCTACCAATGTGAAAAATGTGGCAAAGCTTTTAA 1945
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                                                                                                                     69 AAAGTATTTGCACATATGAAGGGTGTGATAAAGCCTATAATCGACCATCATTATTAGA 128
                                                                                                                                                                                                                                                     129 GCAACATTTAAGAACCCACAGTAATGATCGACCGTATAAATGTACAGTGGACGATTGTGA 188
                                                                                                                                                                                                                                                                                                                                                                                 189 TAAAGCATTTTCAGAAAATCACATTTGGAAACACATATTGTATCACATTCCGAAAAAAA 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       309 TGAAATCACCCATACAAAGTCATTTAAATGTACATTTGAAAATTGTCAAGAAGCATTTTA 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                369 TAAACATCAATCTTTAA---GACATCATATATTATCTGTTCATGAAAAACATTAACGTG 425
Query Match 7.9%; Score 98.2; DB 9; Length 2237; Best Local Similarity 52.0%; Pred. No. 1.6e-06; Matches 273; Conservative 0; Mismatches 243; Indels 9; Gaps
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Search completed: May 9, 2004, 08:56:45 Job time : 5087.84 secs Human tra TRAF6-inh Human ova DNA encod Human cDN

Aca98938 Adc58104 Adc581103 Add31103 Abq81135 Abq85198 Abq55095 Abq55095 Abas69188 I

cDNA

Human gen Human gen Human nov

Abq93353 Acc46324 Acc46373 Acc46373 Abx34443 Aas26690 Abx74049 Abx74040 Aas87125 I

Human dit Human mdd

Human nov DNA encod Human mdd

Human nov Human dit Human cDN DNA encod Human dit Human cod

Abx34772 B Adc30336 B Acc46347 B Adb62883 B Aas67562 D Acc46407 B Ada53516 B

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The present sequence encodes a Candida albicans transcription factor, designated CATFILIA. The polypeptide is a DNA-binding protein, which is fivolved in initiating transcription of the ribosomal RNA SS gene. The polymuclectide is used to screen for its specific inhibitors, potentially useful as antimycotic agents, to raise an antibody response that is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid encoding Candida albicans transcription factor, useful e.g. in screening for antimycotic agents and for immunization.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding a transcription factor designated CATFIIIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transcription factor, CATFIIIA, DNA-binding protein, ribosomal RNA 58 gene, fungal infection, ss.
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/transl_except= (pos:
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P-PSDB; AAY93316.
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WO200028037-A1
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                    GenCore version (c) 1993 - 2004
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Maximum Match 100%
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The invention relates to constructing (M1) a strain of diploid fungal cells in which both alleles of a gene are modified, comprising modifying one allele by insertion or replacement by a cassette having an expressible selectable marker and modifying other allele by recombination, of a promoter replacement fragment with a hererologous promoter. So that expression of the second allele is regulated by the promoter. (M1) is useful for constructing a strain of diploid fungal cells in which both alleles of a gene are modified. The diploid fungal cells in whing both alleles modified are useful for identifying a gene that is essential to the survival or growth of a fungus, a gene that contributes to the virulence and/or pathogenicity of a fungus, a gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Constructing strains for identifying gene products as effective targets for therapeutic intervention, by inactivating in the strain one allele of a gene and placing other allele of the gene under conditional expression.
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1620 GATAGTCTAGATGAAAAAAAGTGATGTTAGATCAGACTCAATGTCAGCTCAAAGATCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fungus; yeast; tetracyclin; promoter; GRACE strain; biosynthesis; signal transduction; DNA replication; cell division; growth; proliferation; Candida albicans; fungicide; antifungal; gene; ss.
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22-AUG-2001; 2001US-0314050P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protective against fungal infection and to raise antibodies. Such antibodies, as well as the polypeptides and polymucleotides are used compositions for diagnosing and treating fungal infections, e.g. by detecting polymorphisms and mutations
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                                                                                                                Length 2060;
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Pred. No. 1e-233;
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Hio Y, Otsuka K, Nagai K, Irie R, Tamechika
Otsuka M, Nagahari K, Masuho Y;
                                                                             ATAAAATCATTTACTGCTTCTTTGGAAGGTTCAAAGAGTGTTTCTAAACTTATTCTGAAT
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24-JAN-2002; 2002US-0350435P
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Seki N, Yos
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agent, an antifungal agent that inhibits the growth of a diploid fungus and for identifying a therapeutic agent for treatment of a mammalian disease. (M.) is useful for identifying a compound which modulates the activity of a gene product, preferably enzymatic activity, carbon compound catabolism, biosynthetic, transporter, transcriptional, translational, signal transduction, DNA replication and cell division activity. The method is useful for identifying a compound having the ability to inhibit growth or proliferation of C albicans cells and for treating infection by C albicans. The present sequence is that of an essential Candida albicans gene used in the method of the invention. Note: The sequence data for this patent is not represented in the printed the contraction by C. Albicans contraction of the invention.
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                                                                                                                                                                                                                                                                99.7%; Score 1232.8; DB 6;
llarity 99.8%; Pred. No. 3.9e-233;
Conservative 0; Mismatches 2;
                                                                                                                                                                                                        European Patent Office
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Best Local Simil
Matches 1234; C
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07-SEP-2001; 2001US-0317912P. 14-SEP-2001; 2001US-032270P. 21-SEP-2001; 2001US-032464P. 28-SEP-2001; 2001US-032732P. 19-CT-2001; 2001US-0346716P. 25-JAN-2002; 2002US-0351749P.

22-FEB-2002; 2002US-0359498P.

2001US-0317792P.

07-SEP-2001;

2002WO-US028540

05-SEP-2002;

20-MAR-2003

WO2003023003-A2 Homo sapiens.

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CATAAGAGAATTCATACTGGAGAAACCCTACCAATGTGAAAAATGTGGCAAAGCTTTT 1737
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              The present invention relates to novel human secretory or membrane proteins (ADA54072-ADA55110) and their coding sequences (ADA52433-ADA54071). The coding sequences are useful in the gene therapy of diseases caused by abnormalities of the proteins, e.g. cancer, inflammatory diseases, osteoporosis or neurological disease.
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                                                                                                                                                                                           Score 99.4; DB 7; Length 2132; Pred. No. 3.4e-10;
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                                                                                                                                                     Sequence 2132 BP; 833 A; 423 C; 347 G; 529 T; 0 U; 0 Other;
                                                                                                                                                                                                                                          0; Mismatches 281; Indels
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50.6%;
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Human, nucleic acid-associated protein, cytostatic, antiarteriosclerotic, anticonvulsant, nootropic, neuroprotective, cerebroprotective, anti-HIV; antialfametory; thyromizetic, gene therapy; cell proliferative disorder, cancer; atherosclerosis, neurological disorder, epilepsy; Huntington's disease; stroke; immune disorder; inflammatory disorder; AIDS; allergy; evelopmental disorder, inflammatory disorder; AIDS; allergy; protein interaction; developmental disorder; hypothyroidism; Cushing's syndrome; infection; gene expression profile; gene; ss.
                                                                                                                              encoding human nucleic acid-associated protein (NAAP) #51
ACA98970 standard; cDNA; 1705
                                                                                      (first entry)
                                                                                                                                     CDNA
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The invention describes a novel human isolated mucleic acid-associated polypeptide (NAAP). The polypeptides and polymucleotides are useful in diagnosing, treating and preventing diseases or conditions associated with the decreased expression or overexpression of NAAP, such as cell proliferative (e.g. cancer, atherosclerosis), neurological (e.g. AlDS, epilepsy, Huntington's disease, stroke), immune/inflammactry (e.g. AlDS, allexyfes) and developmental (e.g. Hypothyroidism, Cushing's syndrome) disorders, or infections. These are also useful in assessing the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of MAAP. The NAAP or its fragments are useful in screening compounds for effectiveness as agonist or antagonist of the polypeptide, or in altering the expression of the target polymucleotide and compounds that specifically bind to or modulate the activity of the polypeptide. The microarray is useful in monitoring or measuring protein-protein interactions, drug-target interactions, and gene expression profiles. This sequence encodes a novel human nucleic acid-associated protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New human nucleic acid associated proteins (NAAP), useful for diagnosing, treating and preventing diseases or conditions associated with the aberrant NAAP expression e.g. cancer, AIDS, atherosclerosis, epilepsy, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 754
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Becha SD, Richardson TW, Lee EA, Sprague WW, Emerling BM;
Thangavelu K, Warren BA, Tran UK, Yue H, Xu Y, Yue H, Li JX;
Hafalia AJA, Sanjanwala B, Marquis JP, Gorvad AE, Lee SY, Iso)
Baughn MR, Chawla NK, Nguyen DB, Swarnakar A, Zebarjadian Y,
Thornton M, Yao MG, Khan FA, Gandhi AR, Yang J, Kable AE;
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Pred. No. 1.1e-09;
0; Mismatches 222;
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Burford N, Ramkumar J;
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The invention relates to a combination which, comprises a number of polymucleotide probes comprising a sequence selected from one of the 1490 sequences mentioned in the specification. The combination is useful as an array element in a microarray for monitoring the expression of a number of target polymucleotides. The microarray is particularly useful in the diagnosis and treatment of cancer and immunopathology and neuropathology. The microarray is useful in diagnostics and treatment regimens, drug discovery and development, toxicological and carcinogenicity studies, monitoring progression of diseases and for developing sophisticated profiles for the effects of currently available therapeutic drugs. The
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signalling pathway population: cancer: adenocarrinom
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combination is also useful for purifying a subpopulation of mRNAs, cDNAs and genomic fragments and in research and diagnostic applications. The array can detect changes in expression in a large number of genes coding for different signaling pathway populations which can be used to diagnose various diseases including cancer e.g. adenocarcinoma and leukaemia, immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease and Parkinson's disease. The present sequence represents a polynucleotide probe of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at
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Wed May 12 12:38:U1 2004

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (FCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal cativity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular waight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving abbarrant protein expression or biological activity. The polypeptide and polynuclectide sequences have applications in disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. Aps64197-AAS94564 represent novel human diagnostic coding sequences. Aps64197-AAS94564 represent novel human diagnostic patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at (II) but was obtained in the way New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forenaics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity. Claim 1; SEQ ID NO 27121; 103pp; English. 30-MAR-2001; 2001WO-US008631 31-MAR-2000; 2000US-00540217, 23-AUG-2000; 2000US-00649167, Drmanac RT, Liu C, 2001-639362/73. (HYSE-) HYSEQ INC. P-PSDB; ABG27130 WO200175067-A2 11-OCT-2001

Sequence 4563 BP; 1752 A; 814 C; 824 G; 1173 T; 0 U; 0 Other;

GGCAAAGCTTTTAGGCAATCCTCACACCTTACTAGACATAAAGCAATTCATACTGGAGAG 1548 1315 GAATGTGGCAAAGCCTTTAACCAGTCCTCACACCTTACTCAACATAAAACÁATTCATACT 1374 1375 GGAGGGAAAACCTACAAATGTGAAGAATGTGGGCAAAGCTTTTAACCATCTTTCAGCCCTT 1434 AAAAAGTATATTTGCACATATGAAGGGTGTGATAAAGCCTATAATCGACCATCATATTA 126 127 GAGCAACATTTAAGAACCCACAGTAATGATCGACGGTATAAATGTACAGTGGACGATTGT 186 GATAAAGCATTTTTCAGAAAATCACATTTGGAAACACATATTGTATCACATTCCGAAAAA 246 247 AAACCATTCCATTGTTCAGTGTGTGGTAAAGGGGTTAATTCTCGACAACACTTGAAAAGA 306 7 GAAAGIGACGAAACCAAAICGATAICAICTITAATAICTICTICTICTICAICACGICCC 66 1435 ACTAAACATAAGATAATTCATACTGGGGAGAAACCATACAAATGT-----GAAGAATGT Gaps ٠. ف 7.7%; Score 95.2; DB 5; Length 4563; 52.7%; Pred. No. 2.5e-09; Live 0; Mismatches 223; Indels 9; Conservative Best Local Similarity Matches 258; Conserv 1489 187 Query Match qq d à g g à ò ò

1729 idigaagaardiggraaagcrirraagreercarcaaaacrracreracaraaggraarr 1788 367 TATAAACATCAATCTTTAAGA---CATCATATATTATCTGTTCATGAAAAAACATTAACG 423 1669 AGCCAGTCCTCAACCCTTAGAAACCATCAGATAATTCATACTGGAGAGAAACCCTACAAA TGTAAACAATGTAATAAAGTTTTCACTCGACCTTCAAAATTAGCACAACATAAAAA 1789 CATACTGGAG 1798 484 CATCATGGTG 424 8 셤 ò g à g

AAL51569

BP AAL51569 standard; DNA; 2597

AAL51569;

(first entry) 10-APR-2003 Human nucleic acid-associated protein coding sequence - SEQ ID No 52.

Human, gene, ds, nucleic acid-associated protein, NAAP, arteriosclerosis, cell proliferative disorder; atherosclerosis; cirrhosis; hepatitis; AIDS, cancer; developmental disorder; renal tubular acidosis; anaemia; asthma, mental retardation; neurological disorder; Alzheimer's disease; epilepsy; Parkinson's disease; autoimune disorder; inflammatory disorder; allergy; Crohn's disease; transgenic animal; animal model.

WO2003000864-A2.

03-JAN-2003

20-JUN-2002; 2002WO-US021179

22-JUN-2001, 2001US-0300518P. 29-JUN-2001, 2001US-0301797P. 29-JUN-2001, 2001US-030192P. 29-JUN-2001, 2001US-0301892P. 29-JUN-2001, 2001US-0301893P. 06-JUL-2001; 2001US-0303405P. 06-JUL-2001; 2001US-0303442P. 15-MAR-2002; 2002US-0364438P. 22-JUN-2001; 29-JUN-2001;

(INCY-) INCYTE GENOMICS INC.

SY; Emerling BM; Forsythe IJ; Gandhi AR, Swarnakar A, Hafalia AJA, Warren BA, Emerling BM; Arvizu CS, Ison CH, Honchell CD, Lee EA, Yue H, Forsythe IJ; Ramkumar J, Griffin JA, Yang U, Sanjamala MM, Baughn MR, Borowsky ML, Yao MG, Walia NK, Bandman O, Lal PG, Becha SD, Richardson TW, Elliott VS, Luo M, Tang YT, Zebarjadian Y, Lu

WPI; 2003-201420/19. P-PSDB; AA016419.

New nucleic acid-associated proteins and polynucleotides, useful for diagnosing, treating or preventing cell proliferative (e.g. cancer), nearrological (e.g. epilepsy or Parkinson's disease), or autoimmune disorders (e.g. AIDS).

Claim 12; Page 292-293; 312pp; English.

The invention comprises the amino acid and coding sequences of human nucleic acid-associated proteins (NAAP). The DNA and protein sequences of the invention are useful for diagnosing, treating or preventing disorders associated with aberrant expression of NAAP, such as: cell proliferative disorders (e.g. arteriosclerosis, atherosclerosis, cirrhosis, hepatitis

AAACCTACAAATGTGAAATGTGGCAAAGCTTTTAACCATTTCTCAGACCTTAGAAGA 1608

307 CATGAAATCACCCATACAAAGTCATTTAAATGTACATTTGAAAATTGTCAAGAAGCATTT 366

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or cancer); developmental disorders (e.g. renal tubular acidosis, anaemia or cancer); neurological disorders (e.g., Alzheimer's disease, Parkinson's disease, Parkinson's disease, Parkinson's disease or epilepsy); and autoimmune/inflammatory disorders (e.g. AlDS, allergies, asthma or Crohn's disease). The DNA sequences of the invention are useful for creating transgenic animals to model human disease. The present DNA sequence encodes a human nucleic acid-associated protein of the invention 886666668888

Sequence 2597 BP; 947 A; 504 C; 505 G; 641 T; 0 U; 0 Other;

1183 TTATAAATGTGAAGAATGTGGCAAAGGCCTTTAATGTGTCCTCAACCCTTACTCAACATAA 1129 1184 TAACGTGTCCTCAACTCTTACTCAACATAAGAGAATTCATACTGGAGAAAAACCATACAA 1243 1244 Arigigaagaarigiggcaaagccrrraacacarccrcacccccaccacaraaaagaar 1303 1304 TCATACCGGAGAGAAACCCTACAAATGTGAAGAATGTGGCAAAGCCTTTAACCAGTTCTC 1363 1364 ACAACTTACTACATAAGATAATTCATACTGGAGAAACCCTACAAATGTAAAGAATG 1423 317 197 257 CCATACAAAGTCATTTAAATGTACATTTGAAAATTGTCAAGAAGCATTTTATAA---ACA 374 434 TAATAAAGTTTTCACTCGACCTTCAAAATTAGCACAACATAAATTAAAACATCATGGTG 493 TTGCACATATGAAGGGTGTGATAAAGCCTATAATCGACCATCATTATTAGAGCAACATTT TTGTTCAGTGTGTGGTAAAGGGGTTAATTCTCGACAAAACACTTGAAAAGACATGAAATCAC TCAATCTTTAAGACATCATATATATCTGTTCATGAAAAAACATTAACGTGTAAACAATG 138 AAGAACCCACAGTAATGATCGACCGTATAAATGTACAGTGGACGATTGTGATAAAGCATT GAGAATTCATACTGGAGAGAAACCTTACAAATGT-----GAAGAGTGTGGCAAAGCCTT Gaps <u>ب</u> Length 2597; Score 94.6; DB 7; Length 2: Pred. No. 3e-09; 0; Mismatches 179; Indels 7.78; Query Match Best Local Similarity 55.1 Matches 231; Conservative 1070 1130 258 318 375 435 78 198 1424 g g ठे ò ò ద ò d ò a δ g ò

RESULT

AAS64586 standard; cDNA; 3639 AAS64586

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AAS64586;

(first entry) 13-FEB-2002

encoding novel human diagnostic protein #390. DNA Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder;

Homo sapiens

11-OCT-2001,

30-MAR-2001; 2001WO-US008631

2000US-00540217 2000US-00649167 31-MAR-2000; 23-AUG-2000;

(HYSE-) HYSEQ INC

Drmanac RT, Liu C,

ΥŢ

Tang

WPI; 2001-639362/73 P-PSDB; ABG00399

New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.

Claim 1; SEQ ID NO 390; 103pp; English.

The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PKT) primers, oligomers, and for chomosome and gene mapping, and in recombinant production of (II). The polymuclectides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal crivity of (II) or to traat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a useful for generating antibodies against it, detecting or quantitating collapseptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymuclectide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and anno acid sequences. AAS64197 AAS64454 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this electronic format directly from WIPO at the printed specification, but was obtained in electronic format directly from WIPO at the fire of sequences.

Sequence 3639 BP; 1403 A; 708 C; 622 G; 906 T; 0 U; 0 Other;

õ Gaps 6 Length 3639; 0; Mismatches 191; Indels Score 92.4; DB 5; Pred. No. 8.6e-09; 7.58; 54.1%; Conservative Similarity 236; Query Match Local

798 TABACATAAGAGAATTCATACTGGAGAAACCCTACAAATGT-----GAAGAATGTGG 851 AAAGTATATTTGCACATATGAAGGGTGTGATAAAGCCTATAATCGACCATCATTATTAGA 852 caaaccririraccccrrcrrcrrcraccrracarcaraacararcaracaraaaaa 129 GCAACATTTAAGAACCCACAGTAATGATGACGTGTATAAATGTACAGTGGACGATTGTGA 189 TAAAGCATTTTTCAGAAAATCACATTTGGAAACACATATTGTATTCACATTCCGAAAAAAA 912 ACCCTACAAATGTAAAGAATGTGGCAAAGCTTTTAGCAATTCCTCAACCTTGGTAATCA 69 738 249 g 셤 셤 셤 ò ઠે $\ddot{\delta}$ ò

taagataactcatactgaagagaaaccctacaaatgtaaagaatctgacaaaccttttaa 1031 309 IGAAATCACCCATACAAAGTCATTTAAATGTACATTTGAAAATTGTCAAGAAGCATTTTA 972 셤

1032 GCGACTCTCAACCCTTACTAAACATAAATAATACATGCTGGAGAAACTCTACAAATG 369 TAAACATCAATC---TTTAAGACATCATATATTATCTGTTCATGAAAAAAACATTAACGTG a

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rgaagaargregcaaagcririraarcgarcricaaarcrracraracaraagrirarrca TAAACAATGTAATAAAGTTTTCACTCGACCTTCAAAATTAGCACAACATAAAACA 1092 g ò

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TCATGGTGGATCTCCT TACTGGAGAGAAACCT 486

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ADB63624 standard; cDNA; ADB63624 ID ADB6 XX RESULT 9

canaccgaagagaacccnacaaangnaaagaangnggcaaagcmmaaacacmccnca 1312

1253 61

CGTCCCAAAAAGTATATTTGCACATATGAAGGGTGTGATAAAGCCTATAATCGACCATCA

120

Human; ss; gene; pharmaceutical; diagnostic; gene therapy; tissue regeneration; cell regeneration; membrane protein; signal transduction-related protein; transcription-related protein; transcription-related protein; osteoporosis; neurological disease; cancer; tumour.

Location/Qualifiers 170. 1792 /*tag= // product = "Clone THYMU20071120 protein"

EP1308459-A2

07-MAY-2003

28-MAR-2002; 2002EP-00007401

2001JP-00379298 2002US-00350978 05-NOV-2001; 25-JAN-2002; (HELI-) HELIX RES INST. (REAS-) RES ASSOC BIOTECHNOLOGY.

Otsuki T, Wakamatsu A, Sato H, Ishii S; Hio Y, Otsuka K, Nagai K, Irie R, Tamechika Otsuka M, Nagahari K, Masuho Y; Isogai T, Sugiyama T, Yamamoto J, Isono Y, Seki N, Yoshikawa T,

WPI; 2003-450961/43. P-PSDB; ADB65594.

New polynuclectides and polypeptides, useful for developing a diagnostic marker or medicines for regulation of their expression and activity, or as targets of gene therapy.

Claim 1; Page; 222pp; English

The invention discloses a polynuclectide comprising a sequence selected from 1970 fully defined nucleotide sequences which encode novel polypeptides. Also claimed is a polypeptide encode by the polynuclectide, a matibody binding to the polypeptide or peptide or the polynuclectide, immunologically assaying the polypeptide or peptide of the polynuclectide by contacting the polypeptide or peptide with the antibody of the encoded protein, and observing the binding between the two, a transformant carrying the polynuclectide in an expressible manner and an antisense polynuclectide. The oligonuclectide is useful as a primer for synthesising the polynuclectide, or as a probe for detecting the polynuclectide. The polynuclectide and encoded is useful as parimer for synthesising the polynuclectide, or as a probe for detecting the polynuclectide. The polynuclectide and encoded as defined in them, for developing a disgnostic marker or medicines for regulation of their expression and activity, or as targets of genes may be included in them, for developing a disgnostic marker or medicines for regulation of their expression and activity, or as targets of genes may be used as indicators for diseases (e.g. osteoporosis, transcription-related proteins, disease-related proteins, and genes encoding them can be used as indicators for diseases (e.g. osteoporosis, neurological diseases, cancer, tunours. The cDNA may be used to regulate the activity or expression of the invention. Note: some of the sequence content is a cDNA of the invention. Note: some of the sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the European Patent Office.

Sequence 2110 BP; 784 A; 394 C; 386 G; 546 T; 0 U; 0 Other;

4. Gaps Query Match

7.4%; Score 91.8; DB 9; Length 2110;
Best Local Similarity 51.7%; Pred. No. 1e-08;
Matches 314; Conservative 0; Mismatches 277; Indels 16;

1486 1546 1666 1366 417 656 477 .607 TACABATGTGABATGTGGCAAAGCTTTTAGCCGATCCTCAAAACTTACTGAACATAAG 1727 iciocadacti-----iacidadearadadadadacaracideadadadeacadadae 1427 GGAAAGAAACCCTACAAATGTGAAGAATGTGGCAAAGCTTTTATCCAATCCTCAAACTT 537 ITTCCAAACTTGGTCAGTATTACAATTTCATATAAAACAACTGCATCCAAAACTTAAATG gecertactacadataagadaatreacadagagagagagagagagagagagagagagagaga-----daa GATTGTGATAAAGCATTTTCAGAAAATCACATTTGGAAACACATATTGTATCACATTCC 1367 GAATGTGGGAAAGCTTTTAACCGATCCTCAAAACTTACTGAACATAAGAAACTTCATACT GAAAAAAAAACCATTCCATTGTTCAGTGTGTGAAAGGGGGTTAATTCTCGACAACACTTG 1487 Actgaacataaaaaaatrcatrcrgagagagaaaacccracaagrgrgaagaargrggggaaa GCATTITATAAACATCAATCTTTA---AGACATCATATATTATCTGTTCATGAAAAAAA 1547 derritradacacececeratecerraceacaradadaaracaracerracegadadadeec 1667 ATAATTCATACTGGAGAGAACCCTATAAATGTGAGAGATGTGACAAAGCTTTTAACCAA TTATTAGAGCAACATTTAAGAACCCACAGTAATGATCGACCGTATAAATGTACAGTGGAC AAAAGACATGAAATCACCCATACAAAGTCATTTAAATGTACATTTGAAAATTGTCAAGAA 418 ITAACGIGIAAAACAAIGIAATAAAGITITICACICGACCITCAAAATIAGCACAAAAAAAA 597 TCCTAAATGTGGGTAAAGGTTGTGTTGGGAAAAAAGGTTTATCTTCACATATGTTAAGTCA 1841 TACTGGT 1847 657 TGATGAT 663 121 1313 241 301 361 181 셤 ŝ g ò g ò g ò g ઠે 엄 $\stackrel{\circ}{\sigma}$ 셤 ò 셤 8 g ઠે g ઠે

BP. ADC56695 standard; cDNA; 2760 Human macroprotein-45-76 cDNA (first entry) 18-DEC-2003 ADC56695 RESULT 10

macroprotein-45.76; dementia; arrhythmia; asthma; diabetes; ss; human;

Homo sapiens.

Location/Qualifiers 180. .1430 147-tag= "Human macroprotein-45.76" /product= "Human macroprotein-45.76"

CN1382725-A

04-DEC-2002

26-APR-2001; 2001CN-00112764

26-APR-2001; 2001CN-00112764

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The invention discloses a polymucleotide comprising a sequence selected from 1970 fully defined nucleotide sequences which encoded novel colypoptides. Also claimed is a polypoptide encoded by the polymucleotide, an antibody binding to the polypoptide or peptide or its partial peptide, an antibody binding to the polypoptide or peptide or the polymucleotide, immunologically assaying the polypoptide or peptide or peptide by contexting the polypoptide or peptide with the antibody of the encoded protein, and observing the binding between the two, a transformant carrying the polymucleotide in an expressible manner and an antisense polymucleotide. The oligonucleotide is useful as a primer for synthesishing the polymucleotide, or as a probe of contecting are useful as pharmaceutical agents and encoded proteins are useful as pharmaceutical agents and many disease-related proteins are useful as pharmaceutical agents and many disease-related configuration of their expression and activity, or as targets or genes are involved in tissue and/or call configuration. Membrane proteins, aignal transduction-related proteins, contending them can be used as indicators for diseases (e.g. osteoporosis, convolvity or expression of the encoded proteins and genes are convolved in tissue content of seases, cancer, tumours. The cDNA may be used to regulate the activity or expression of the encoded protein to treat diseases. The convolvity or expression of the encoded protein to treat diseases. The sequence presented is a cDNA of the invention. Note: Some of the sequence of sease of the protein or the printed specification, but is based on sequence information supplied by the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polynucleotides and polypeptides, useful for developing a diagnostic
marker or medicines for regulation of their expression and activity, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71 AGIATATTIGCACATATGAAGGGTGTGATAAAGCCTATAATCGACCATCATTATTAGAGC
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tissue regeneration, cell regeneration; membrane protein;
signal transduction-related protein; transcription-related protein;
osteoporosis; neurological disease; cancer; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.4%; Score 91.8; DB 9; Length 3078; 52.1%; Pred. No. 1.1e-08; ve 0; Mismatches 227; Indels 9;
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Hio Y, Otsuka K, Nagai K, Irie R,
Otsuka M, Nagahari K, Masuho Y;
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                                                                                                                                                                   "Clone FEBRA20063720 protein"
                                                                                                          Location/Qualifiers
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(REAS-) RES ASSOC BIOTECHNOLOGY.
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25-JAN-2002; 2002US-00350978.
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Seki N, Yoshikawa T,
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P-PSDB; ADB64438.
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                                                                                                                                                                                                                                           The invention relates to a novel human macroprotein-45.76, the encoding polynucleotide, an antagonist and a method of recombinant production. The protein of the invention may be useful for treating dementia, arrhythmia, asthma and diabetes. The current sequence is that of the human macroprotein-45.76 cDNA of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70
                                                                                                                                New human macroprotein-45.76, encoding polynucleotide, antagonist and recombinant production, useful for treating dementia, arrhythmia, asthma
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                                                                                                                                                                                                                                                                                                                                                                                                  7.4%; Score 91.8; DB 9; Length 27. Local Similarity 52.1%; Pred. No. 1.1e-08; tes 257; Conservative 0; Mismatches 227; Indels
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Burford N,
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                                                                                                                                                                                                                                                                                                                                                                     AACATTTAAGAACCCACAGTAATGATCGACCGTATAAATGTACAGTGGACGATTGTGATA 190
                                                                                                                                                  AAGCITITIAACCGGICCICAAAICITACIAAACAIAAAATAAITCATACIGGAGAAAAC 883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; nucleic acid associated protein; NAAP; stroke; AIDS; nootropic; cancer; atherosclerosis; neurological; epilepsy; Huntington's disease; developmental disorder; antiinflammatory; neuroprotective; thyromimetic; cushing's syndrome; infection; gene therapy; cytostatic; anticonvulsant; cerebroprotective; hypothyroidism; cell proliferative disorder; allergy;
                                                                                                              AACAATGTAATAAAGTTTTCACTCGACCTTCAAAATTAGCACAACATAAAATTAAAACATC
                                                                  AACATAAGATAATTCATACTGGAGAAAACCCTACAAATGT-----GAAGAATGTGGCA
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Lu DAM, Forsythe IJ;
Sanjanwala MM, Lee ]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human nucleic acid associated protein (NAAP)-34 cDNA
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126. 1973
|*tag= a /
/product= "Human NAAP protein"
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BM, Lal PG,
D, Duggan BM,
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13-JUL-2001; 2001US-0305304P.

13-JUL-2001; 2001US-0305390P.

13-JUL-2001; 2001US-0305390P.

20-JUL-2001; 2001US-0306960P.

20-JUL-2001; 2001US-030694P.

27-JUL-2001; 2001US-0306170P.
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Yue H, Baughn MR, Emerling BM
Ramkumar J, Li JX, Becha SD,
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                                                                                                                                                                                                                           New human nucleic acid associated proteins (NAAP), useful for diagnosing, treating and preventing diseases or conditions associated with the aberrant NAAP expression e.g. cancer, AIDS, atherosclerosis, epilepsy, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to human nucleic acid associated proteins (NAAP) and their corresponding nucleic acid sequences. The invention is useful in diagnosing, treating and preventing diseases or conditions associated with the decreased expression or overexpression of NAAP, such as cell proliferative (e.g. cancer, atherosclerosis), neurological (e.g. proliferative (e.g. cancer, atherosclerosis), neurological (e.g. allosympless), and developmental (e.g. Hypothyroidism, Cubhing's syndrome) disorders, or infections. It is also useful in assessing the effects of syngences or infections. It fragments are useful in screening compounds for which acts as their agonist or anteagonist. The microarray compounds for which acts as their agonist or anteagonist. The microarray target interactions, and gene expression profiles. NAAP DNA is used in gene therapy. The present sequence is human NAAP CDNA
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Yao MG;
Lu Y;
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7.3%; Score 90.4; DB 7; Length 2
Best Local Similarity 51.8%; Pred. No. 2e-08;
Matches 258; Conservative 0; Mismatches 231; Indels
      Borowsky ML,
Nguyen DB,
   VS, Ison CH, Ding L, Bo
Walia NK, Hafalia AJA,
                                                                                                                                                                                                                                                                                                                                                                                                 Claim 5; Page 259-260; 260pp; English
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;, Tamechika I;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic; Gene Therapy; human; secretory protein; membrane proteins; cancer; inflammatory disease; gene; ss.
                                                                                                                       1378 aahgrgrchrcacaccrhachcacahaadahgahrcahachggagagaaacchacaaa
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                                                                        367 TATAAACAT---CAATCTTTAAGACATCATATATTATCTGTTCATGAAAAAACATTAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to novel human secretory or membrane proteins (ADAS4072-ADAS5710) and their coding sequences (ADAS2433-ADAS4071). The coding sequences are useful in the gene therapy of diseases caused by abnormalities of the proteins, e.g. cancer, inflammatory diseases, osteoporosis or neurological disease.
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7.3%; Score 90.2; DB 7; Length 2230;
Best Local Similarity 50.4%; Pred. No. 2.2e-08;
Matches 332; Conservative 0; Mismatches 313; Indels 14;
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Hio Y, Otsuka K, Nagai K, Irie
Otsuka M, Nagahari K, Masuho Y;
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                                                                                                                                                                                                                                                                         484 CATCATGGTGGATCTCCT 501
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24-JAN-2002; 2002US-0350435P.
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J, Isono Y, H
Yoshikawa T, O
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Seki N,
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Hio Y, Otsuka K, Nagai K, Irie R, Tamechika
Otsuka M, Nagahari K, Masuho Y;
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7.3%; Score 90.4; DB 7; Length 2114;
Best Local Similarity 51.8%; Pred. No. 2e-08;
Matches 258; Conservative 0; Mismatches 231; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2114 BP; 717 A; 439 C; 434 G; 524 T; 0 U; 0 Other;
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                                                                                                                                                                                   Human coding sequence, SEQ ID 692
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RES ASSOC BIOTECHNOLOGY.
                                         ADA53124 standard; cDNA; 2114
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Yamamoto J, Isono Y,
Seki N, Yoshikawa T,
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                                                                                     ADA53124;
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1245 950 chrahgaratrcaractrcaagagaaacccracaahigrgaacargiggggaaggrerr 1009 .010 AAGCAGTCCCCAACCCTTACTAAACATCAGATAATTTATACTGGAGGGAACCATACAAA 1069 1070 igigadgakarginggaskakacirirrakacirirakakacirracingakakara 1129 1130 TACACTAGAGAGAAAAGCCTACAAATGTGAAAAGGCGAAAGCCTTTAACCAGTTTTCA 1189 542 602 366 367 TATAAACATCAATC---TITTAAGACATCATATATTATCTGTTCATGAAAAACATTAACG 423 AGAGAGATTTCTACAAATGTGAAGAGTGTGGAAAAACCTTTAACTGGTCCACAAAACCTT 775 AAACCATTCCATTGTTCAGTGTGTGGTAAAGGGGGTTAATTCTCGACAACACTTGAAAAGA 306 890 AAACCCTATAAATGTGCACACTGTGGCAAAGCCTTTAAACAGTCCTCACACACTTACTAGA 949 ATGTGGCAGAGCTTTTAACCAGTCCGCAAAGCTCACTGAACATAAGTTAATTCATACTG 1304 AAAAAGTATATTTGCACATATGAAGGGTGTGATAAAGCCTATAATCGACCATCATTATTA 126 661 1190 accerratracacaraagaraarrearagegagagagagagace----eacaarergaaga 776 rcraaactaagaaarrcaractggagaaaacccracaargrgaagra----fGr GATAAAGCATTTTTCAGAAAATCACATTTGGAAACACATATTGTATCACATTCCGAAAAA 830 GGAAAAGCCTTTCACCAATCCTCAATCCTTACTAAACATAAGATAATTCGTACTGGAGAA CATGAAATCACCCCATACAAGTCATTTAAATGTACATTTGAAAATTGTCAAGAAGCATTT TGTAAACAATGTAATAAAGTTTTCACTCGACCTTCAAAATTAGCACAAACATAAATTAAAA 484 CATCATGGTG-GATCTCCTGCTTATCAATGTGATCATCTGGTTGTTTTAAAAATTTCCA 543 AACTIGGICAGIAITACAATITCAIATAAAACAACTGCATCCAAAACTIAAAIGICCIAA 127 GAGCAACATTTAAGAACCCACAGTAATGATCGACCGTATAAATGTACAGTGGACGATTGT ATGTGGTAAAAGGTTGTGTTGGGAAAAAAGGTTTAATCTTCACATATGTTAAGTCATGATG 307 424 603 63 셤 g ò q 원 g ò ò 유 ò ઠે à ठ ò ઠે g g

CDNA sequence, SEQ ID NO:844 ВР ADC30762 standard; cDNA; 2064 (first entry) novel 18-DEC-2003 ADC30762 RESULT

Human; diagnostic; drug screening; forensics; gene mapping; biodiversity assessment; Parkinson's disease; Altheimer's disease; neurodegenerative disease; anemaia; platelet disorder; wound; burns; ulcers; osteoporosis; autoimmune disease; cancer; molecular weight marker; food supplement; antiparkinsonian; nootropic; melvoprotective; antidoagulant; thrombolytic; vulnerary; antilice; osteopathic; immunosuppressive; antiliflammatory; cytostatic; gene therapy; chromosome 19412; gene; ss.

WO2003029271-A2 Homo

24-SEP-2002; 2002WO-US030474. 24-SEP-2001; 2001US-0324631P. 10-APR-2003

Wehrman ٦, Wang QA, Zhao ΑJ, Xue Œ, Ren Zhang J, Tang TY,

(HYSE-) HYSEQ INC.

The invention relates to 971 novel human cDNA sequences (ADC29919-ADC1989) and the polypeptides they encode (ADC30890-ADC1980). The invention also relates to mucleic acid sequences over 99% identical with invention also relates to mucleic acid sequences over 99% identical with invention also relates to mucleic acid sequences over 99% identical with convention and host cells comprising a mucleic acid of the invention; the vectors and host cells polypeptide of the invention; an antibody acid against a polypeptide of the invention; an antibody identifying a compound which binds to a polypeptide of the invention. The identifying a compound which binds to a polypeptide of the invention. The invention further discloses methods of peventing, treating or ameliorating a medical condition; kits comprising polymucleotide probes and/or monoclonal antibodies for carrying out the methods of the invention methods for the identification of compounds that mediate the and/or monoclonal antibodies for carrying out the methods of the invention are conting sequences corresponding to the compounds that mediate the expression or activity of the polymelication of compounds of the invention are conting sequences corresponding to the compounds of the invention are useful in diagnostics, drug screening, fornesics, gene mapping, in the identification of mutations responsable for genetic disorders or other identification of mutations responsable for genetic disorders or other disease and other neurodegenerative disease, and other neurodegenerative disease, and other neurodegenerative diseases, anaemia, platelet disease becomes and other neurodegenerative disease, and other neurodegenerative disease, and other neurodegenerative disease, and other neurodegenerative disease, and other neurodegenerative disease, and other neurodegenerative disease, and other neurodegenerative disease, and other neurodegenerative disease, and other neurodegenerative disease, and other neurodegenerative disease, and other neurodegenerative disease, and other neu New polynucleotide and polypeptide useful for diagnosing, preventing or treating conditions such as neurodegenerative diseases, anemias, platelet disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or ö 7 Wang > Asundi Claim 1; SEQ ID NO 844; 1185pp; English. **,** Wang D, Ma Drmanac RT; 2003-371981/35 Zhou P, Ghosh M, Haley-Vicente D, P-PSDB; ADC31733 WPI;

Sequence 2064 BP; 703 A; 375 C; 449 G; 537 T; 0 U; 0 Other;

942 caagectricagacerearricacaccreecraecaratririararreacaereeaeaaa 1001 1002 ACCTTACAAGTGTAATGAGTGTGGCAAGACCTTTGTTCAAAATTCATCTTGTAATGCA 1061 188 887 888 AAGACATAGGAGAATTCATACTGGAGAAACCGTACAAATGTAAGGT-----TTGTGA 249 ACCATTCCATTGTTCAGTGTGTGGTAAAGGGGTTAATTCTCGACAACACTTGAAAAGACA 309 TGAAATCACCCATAC---AAAGTCATTTAAATGTACATTTGAAAATTGTCAAGAAGCATT .062 raaggricarracragagagagaaargriracaagrgraargaargragacaaggrrrrraa TTATAAACATCAATCTTTAAGACATCATATATTATCTGTTCATGAAAAAACATTAACGTG <u>AAAGTATATTTGGACATATGAAGGGTGTGATAAAGCCTATAATCGACCATCATTATTAGA</u> GCAACATTTAAGAACCCACAGTAATGATCGACGGTATAAATGTACAGTGGACGATTGTGA 189 TAAAGCATTTTTCAGAAATCACATTTGGAAACACATATTGTATCACATTCCGAAAAAA Query Match
7.2%; Score 89.2; DB 9; Length 2064;
Best Local Similarity 53.7%; Pred. No. 3.4e-08;
Matches 234; Conservative 0; Mismatches 193; Indels 9; 69 328 129 366

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Db 1122 TCACAAATCTAGATGTCATCATAGACTTCATACTGGAGAAACCTTACAAGTG 1181

CY 426 TAAACAATGTAATAAAGTTTTCACTCGACCTTCAAAATTAGCACAAACATAAAAAA 485

Db 1182 TAATGAATGTGGCAAGGTTTTTAATTGAAAATCAAACCTTGAACATCATAAGAGTTCA 1241

OY 486 TCATGGTGGATTTTTAATTGAAAATCAAACCTTGAACATCATCATAGAGTTCA 1241
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Search completed: May 9, 2004, 06:07:03 Job time : 557.339 secs

Perfect score: Sequence: Scoring table:

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Searched:

Database

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BZ298000 628 bp DNA linear GSS 31-OCT-2002 CG3957.fl Candida glabrata Random Genomic Library Candida glabrata genomic clone CG3957, genomic survey sequence.
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Saccharomycetales; mitosporic Saccharomycetales;
Saccharomycetales; mitosporic Saccharomycetales; Candida.

J (bases I to 628)
Wong, S., Fares, M.A., Zimmermann, W., Butler, G. and Wolfe, K.H.
Evidence from comparative genomics for a complete sexual cycle in
the 'asexual' pathogenic yeast Candida glabrata
Genome Biol. 4 (2), R10 (2003)
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Contact: Wong S
Contact: Wong S
Trinity College Dublin
Dublin 2, Ireland
Tel: 353 1 6082319
Fax: 353 1 679858
Email: swong@tcd.ie
Class: plasmid ends.
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BC028252
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BC032590
AL705393
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Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                    ATACGATAATTGTGACAAGGCCTTTACAAGGCCGTCCTTGCTCACAGAACACAGAATAC 566
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[ (base 1 to 959) Saccharomycetaceae; Saccharomyces.
Souciet, J. L., Aigle, M., Artiguenave, F., Blandin, G.,
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Malpertuy, A., Neuvelise, C., Ozier-Kalogeropoulos, O., Potier, S.,
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VERSION
KEYWORDS
SOURCE
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AUTHORS
                                                                                                                                                                                                                                          Matches
FEATURES
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Direct Submission

Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,

2 rue Gaaton Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail:

seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces

exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces Kluyveromyces themotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ij
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  899
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(<71. .>958)
/note="similar to Saccharomyces cerevisiae ORF YPR186c
PZF1 ; TFIIIA (transcription initiation factor) ]"
/evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    898 GGTAAAAGGTGTTACTACAAAGCAGCAGTTAAAAAGACATGAGATCACACATACCAAATCG
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                             οĘ
                                                                                                                                                                                2 (bases 1 to 959)
Neuveglise,C., Bon,E., Lepingle,A., Wincker,F., Artiguenave,F.,
Gaillardin,C. and Casaregola,S.
Genomic exploration of the hemiascomycetous yeasts: 9.
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                             set
Wincker, P. and Weissenbach, J.
Genomic exploration of the hemiascomycetous yeasts: 1. A.
yeast species for molecular evolution studies
FEBS Lett. 487 (1), 3-12 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.6%; Score 167.6; DB 29;
ilarity 57.2%; Pred. No. 1.7e-21;
Conservative 1; Mismatches 235;
                                                                                                                                                                                                                                                                                                     Saccharomyces kluyveri
FEBS Lett. 487 (1), 56-60 (2000)
20584719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
/strain="CBS 3082"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:4934"
/clone="AU0AA005F10"
/clone_lib="AU0AA"
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Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Mateuyama, T., Miyazaki, A., Murata, M., Nakain, C., Sakai, R.,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                foodom start=1
/protein id="BAC27766.1"
/protein id="BAC27766.1"
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/brotein id="BAC27766.1"
/translation="MLETYRNINAVGYNWEDSNIEBHCESSRRHGRHERNHTGEKPYE
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GGGARPTQHBSHKIHWYHTGEKPYKCNBCGRAFARHSBLKVHKITHTGEKFYKCDQC
NKARYYESYLQWHKKTHTGEKPYKCNBCGRAFARHSBLKVHKITHTGEKFYKCNQCGR
ALAYHSTLQVHQRTHTGEKPYECEQCGKAFANQSYFQVHKRIHTGEKPYKCDQCGKAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'tissue type="olfactory brain"
'clone lib="RIKEN full-length enriched mouse cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (FRAGMENT) homolog FASTY, 87.1%ID,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              521 ACATACTGGAGAGAAAGGCTACAATGCAATCAATGTGATAAAGGCTATTCACGACACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     635 TCAATGTGGTAAAGCCTTTACACAACACAGTCATCTCAAAATACATATGGTTACACATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 ACGICCCAAAAAGIAIAITIGCACAIAIGAAGGGIGIGAIAAAGCCIAIAAAICGACCAIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          581 CATTCTACAAATACATAAAAGAACACATAGTGGAGAGAAACCCTATGAATGTA----A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="unnamed protein product; MSZF33
[Mus musculus] (SPTR|088251, evidence:
100%length, match=255)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prepare mouse tissues.
Please visit our web site for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="FANTOM_DB:6430503015"
/db_xref="MGI:335676"
/db_xref="taxon:10090"
/clone="6430503015"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .1609
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/64"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VGSSDLKRHERVHTGRETLQM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dev stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         outative
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tes 310; Conserv
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Matches
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MRNA linear HTC 18-SEP-2003

Mus musculus adult male olfactory brain cDNA, RIKEN full-length
enriched library, clone: 6430503015 product: MSZF33 (FRAGMENT)
homolog [Mus musculus], full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishi, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Masumoto, R., Hazama, M., Isepami, T., Kashiwagi, K., Yamamoto, R., Inguwa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKD integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genes
                                        624
                                                                                                   cararcaagecegaccarccaageriecacrerarancerarerecaagecrierereger 539
                                                                                                                                                                             625 AAAAAAGTTTATCTTCACATATGTTAAGTCATGATGATTCTACCATGATCAAAATATGG 684
                                                                                                                                                                                                                                           479
                                                                                                                                                                                                                                                                                                                 ACTIGIGATIATIGIGATGIGGGGAAATTIGCAAAGAAAAAGAAATTAGITGAACATTAT 744
                                                                                                                                                                                                                                                                                                                                                                                       478 AAATGTACCATTTGTCAGCAAGTCTCTTTTGCTAAGAAGGCTGATCTTTTATCTCACTAC 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 tull-length cDNAs

Nature 420, 563-573 (2008)

6 (bases 1 to 1609)

8 Addhi,J., Alzawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P. Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Haragaki,T., Harada,X., Hashizume,W., Harasu,M., Kagawa,I., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kagukawa,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the RIKEN Genome Exploration Research Group Phase II Team and the
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                                                                                                                                                                                                                                           GAGTCTGGTCTACAGATGCACATGCGAGTCCATGACGAGGCTTTAGTAATAAAATTGG
                                    CATATAAAACAACTGCATCCAAAACTTAAATGTCCTAAATGTGGGTAAAGGTTGTGTTGGG
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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HTC; CAP trapper.
Mus musculus (house mouse)
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NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki
CDNA Library Preparation: I.M.A.G.E. Consortium (LLNL)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site:
http://www.shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
R. M.
                                                                                                                                                                                                                                                                 Genome
CA 94305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1235 GAATGIGGCAAAACTTTTAACCGATTCTCAACTCTTACTACCCATAAGATAATTCATACT 1294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1409 GGCAAAGCCTTTAAAGCAGTCCTCAAACCTTACTACATAAGATAATTCATACTGGAGAG 1468
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Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2599,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGTAAACAATGTAATAAAGTTTTCACTCGACCTTCAAAATTAGCACAAAATAAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1295 ggagagagagccracaarteraaagaargragagagagcrirraaccgarcrircaacccrr
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50.1%; Pred. No. 1.7e-08;
tive 0; Mismatches 317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4828290"
/tissue_type="Testis"
/clone_lib="NIH MGC_97"
/lab_host="DH10B"
/note="UH00B"
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M.D. Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Homo sapiens zinc finger protein 85 (HPF4, HTF1), mRNA (cDNA clone MAGE:4828290), with apparent retained intron.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTAAAAACATCATGGTGGATCTCCTGCTTATCAATGTGATCATCTCGGTTGTTTTAAAAA 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           537 TITCCAAACTIGGTCAGIATIACAAITTCATATAAAACAACTGCAICCAAAACTTAAATG 596
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                                                                                                                                                                                                                    AGCATTT --- TATAAACATCAATCTTAAGACATCATATATTATCTGTTCATGAAAAAC 416
                                                                                                                                                                                                                                                                         AGCCTTTGTATATGAAAGTTATTTACAAGTTCATAAAAAAACACATACTGGAGAAACC 874
                                                                                                                                                                                                                                                                                                                            ATTAACGIGIAAACAAIGIAAIAAAGIITIICACICGACCIICAAAAIIAGCACAACAIAA 476
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2647)
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Submitted (03-MAR-2003) National Institutes of Health, Mammalian
                                                           TGGAGAGAAACCTTACAAATGTAATCAATGTGGTAAAGCCTTTGCATGTCATAATAAACT
                                                                                                                 GAAAAGACATGAAATCACCCATACAAAGTCATTTAAATGTACATTTGAAAATTGTCAAGA
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I (basea I to 745)
Ota, T., Wakamatsu, A., Ozawa, M., Ishii, S., Saito, K., Yamamoto, J., Nakamura, Y., Nishikawa, T., Nagai, T., Suzuki, Y., Sugano, S. and HRI human cDNA project (Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S., Saito,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano,S., Isogai,T.)
Unpublished (2000)
Contact: Takao Isogai Email: genomicsehri.co.jp
HRI human cDNA project, 5'- & 3'-end one pass sequencing: Helix
Research Institute, cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
Location/Qualifiers 87 gaangiggcaaaactrirraaccgarccicaacrciraciaccaraagaraarrcaracr 127 GAGCAACATTTAAGAACCCACAGTAATGATCGACCGTATAAATGTACAGTGGACGATTGT 7 GAAAGTGACGAAACCAAATCGATATCATCTTTAATATCTTCTTCTTCTTCATCACGTCCC 67 AAAAAGTATATTTGCACATATGAAGGGTGTGATAAAGCCTATAATCGACCATCATTATTA Gabs TGTGGTAAAGGTTGTGGGAAAAAAGGTTTATCTTCACATATGTTAAGTCATGATGA 12; Length 745; Similarity 50.2%; Score 97.6; DB 9; Length 74 Similarity 50.2%; Pred. No. 2.1e-08; Pred. No. 2.1e-08; Conservative 0; Mismatches 314; Indels Genomics Laboratory Helix Research Institute 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan Tel: 81-438-52-3975 Fax: 81-438-52-3986 AUÎ23448 AUI23448.1 GI:10948164 Homo sapiens (human) 328; Conservative Homo sapiens sogai, T. Query Match Best Local S: Matches 328 187 1769 604 RESULT 5 AU123448 LOCUS DEFINITION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS JOURNAL COMMENT ACCESSION FEATURES TITLE g ô g g ò ò g ò g

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Homo sapiens zinc finger protein 85 (HPF4, HTF1), mRNA (CDNA clone IMAGE:5259399), containing frame-shift errors.
BC036394
BC036394.1 G1:23025784 Submitted (05-AUG-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA NIH-MGC Project URL: http://mgc.nci.nih.gov (bases 1 to 2672) Homo sapiens (human) Strausberg, R. Direct Submission 12477932

COMMENT

Shiraki Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Sh
CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Sh
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
http://www.systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anurad
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting MGC help desk

ORGANISM

SOURCE

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 73 Row: a Column: 16 This clone has the following problem: frame shifted. Location/Qualifiers

FEATURES

/mol type="mmkn,"
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/clone lib="nHH MGC_95"
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9; Gaps Query Match 7.5%; Score 92.4; DB 11; Length 2672; Best Local Similarity 54.1%; Pred. No. 1.7e-07; Matches 236; Conservative 0; Mismatches 191; Indels 9; Query Match

ORIGIN

1745 AGAGAAGCCTTACAAATGTAAAGAATGTGAAAAGCTTTTAACCAATCCTCAAAACTTAC 1804 1805 TGAACATAAGAAAATTCATACTGGAGAGAAACCCTATGAATGT-----GAAAATGTGG 1858 AAAGTATATTTGCACATATGAAGGGTGTGATAAAGCCTATAATCGACCATCATTAGTA 128 129 GCAACATTTAAGAACCCACAGTAATGATCGACCGTATAAATGTACAGTGGACGATTGTGA 188 189 TAAAGCATTTTTCAGAAAATCACATTTGGAAACACATATTGTATCACATTCCGAAAAAAA ò g ò 임 ò

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1919 ACCITACAAATGIGAAGAATGIGGGAAAGGITTITAAATGGCCCTCAACCCTTACTATCCA 1978 309 IGAAATCACCATACAAAGTCATTTAAATGTACATTTGAAAATTGTCAAGAAGCATTTTA 1979 TAAGATAATTCATACTGGAGAAACCATACAAATGTGAAGAATGTGGCAAAGCTTTTAA

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2099 IGAAGAAIGIGGCAAAGCCITITAACCAGICCICAAACCTIACIAAACAIAAGAGAATICA 2158 426 TAPACAATGTAATAAAGTTTTCACTCGACCTTCAAAATTAGCACAACATAAATTAAAACA ò g

2039 CCAATCCTCAAACTTACCAACATAAAAATTCATACTGGAGAAAACCCTACACATG 2098

369 TAAA---CATCAATCTTTAAGACATCATATATTATCTGTTCATGAAAAACATTAACGTG

2159 TACTGGAGAAAAACCT 2174 486 TCATGGTGGATCTCCT 501 ò

AQ005136 LOCUS DEFINITION RESULT 7

AQ005136 591 bp DNA linear GSS 27-JUN-1998 CIT-HSP-2290017.TF CIT-HSP Homo sapiens genomic clone 2290017, genomic survey sequence. AQ005136 AQ005136 GI:3082581 GI:3082581

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Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammallar; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 591)

RS Adams, M. D., Rounaley, S. D., Zhao, S., Field, C. B., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, B., Wible, C., Shizuya, H., Shoon, M. and Vencer, J.C.

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NL Unpublished (1998) http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html Seg primer: M13-21; Class: BAC ends. /cell_type="Sperm" /clone_lib="CIT-HSP" /note="Vector: pBeloBAC11; Site_1: HindIII; Site_2: organism="Homo sapiens' /mol_type="genomic_DNA" /db_xref="GDB:7150844" /db_xref="taxon:9606" /clone="2290017" Socation/Qualifiers /sex="Male" REFERENCE AUTHORS JOURNAL FEATURES TITLE

ORIGIN

٠, ذ 69 GAÁTGTGGCAAAGCCTTCTACCATTCTTCACCCTTACTACACATAAGGTAATTCATACT 128 67 AAAAAGTATATTGCACATATGAAGGGTGTGATAAAGCCTATAATCGACCATCATTATTA 126 129 GGAGAGAAGCCCTTCAAATGTGAAAAGATGTGAAAGCTTTTAACCACCCTTCAGCCCTT 188 127 GAGCAACATTTAAGAACCCACAGTAATGATCGACCGTATAAATGTACAGTGGACGATTGT 186 189 ACTACACATAAGTTCATTCATGTTAAAGAAAAACCCTACAAATGT-----GAAGAATGT 242 187 GATAAAGCATTTTTCAGAAAATCACATTTTGGAAACACATATTGTATCACATTCCGAAAAA 246 303 AAATCTTACAAATGTGAACAATGTGGCAAAGGCTTTAAACTGGTCTTCAACCCTTACAAAA 362 307 CATGAAATCACCCATACAAGTCATTTAAATGTACATTTGAAAATTGTCAAGAAGCATTT 366 363 CATAAAAGAATTCATACTGGAGAGAAACCCTACAAATGTGAAGAATGTGGCAAAGCCTTT 422 367 TATAAACAT---CAATCTTTAAGACATCATATATTATCTGTTCATGAAAAAACATTAACG 423 423 AATGTGTCTTCACACCTTACTACACATAAGATGATTCATACTGGAGAGAAACCCTACAAA 482 424 TGTAAACAATGTAATAAAGTTTTCACTCGACCTTCAAAATTAGCACAACATAAATTAAAA 483 7 GAAAGTGACGAAACCAAATCGATATCATCTTTAATATCTTCTTCTTCATCACGTCCC Length 591; tch 7.4%; Score 92; DB 28; Length 59 al Similarity 52.2%; Pred. No. 2.4e-07; 256; Conservative 0; Mismatches 225; Indels Query Match Matches 셤 a g g g g ð ò ਨੇ à ò ò 쉼 à

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Contact: Genoscope

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Introduction about this elugier, sequence cluster 9703.f For
more information about this cluster, sequence cluster 9703.f. Contact cgi-bin/cluster.cgi?seq=CSGCAP001DB06QP1&cluster=9703.f. Contact cgi-bin/cluster.cgi?seq=CSGCAP001DB06QP1.
Franday Avenue Genoscope sequence ID : CS0CAP001DB06QP1.

Faraday Avenue Genoscope sequence ID : CS0CAP001DB06QP1.
                                                                                                                                                                                                                                                                                 BX414627 Homo sapiens THYMUS Homo sapiens cDNA clone CSOCAP001YD12 5-FRYRM, mkNA sequence.

BX414627.1 GI:30649903
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                                                           341 CCAGTCCTCAACTCTTAGAAAAAATGAGATAATTCATACTGGAGAGAAACCCTACAAATG 400
                                                                                               426 TAAACAATGTAATAAAGTTTTCACTCGACCTTCAAAATTAGCACAAAATTAAAAATAAAAAA 485
                                                                                                               401 IGAAGAATGIGGIAAAGCITITIAAGTGGICCICAAAACITACIGIACATAAGGIAATICA 460
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished (2001)
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Best Local Similarity 50.1%; Pred. No. 3.5e-07;
Matches 289; Conservative 8; Mismatches 268; Indels 12; Gaps
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HindIII
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1. 593
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B99387.1 GI:3027197
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                     484 CATCATGGTG 493
                                                543 CATACTGGAG 552
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Strausberg, L.C., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausherg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausherg, R.L., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Klausher, R.L., Zeeberg, B., Buetow, K.H., Schefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.L., Wang, J., Hsieh, F.,
Diatchenko, L., Marushana, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Staplecon, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninch, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Norey, K.C., Male, S., Gunaratne, P.H., Richards, S.,
Norley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, B., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Butterfield, Y.S., Krzywinsk, M. Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinsk, M. I., Skalska, U., Smailus, D.E.,
Generation and initial analysis of more than 15,000 full-length
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Homo sapiens hypothetical protein LOC148206, mRNA (cDNA clone LMACE:4797857), containing frame-shift errors.
269 GTGGTAAAGGGGTTAATTCTCGACAACACTTGAAAAGACATGAAATCACCCATACAAAGT 328
                                                                                                                          329 CATTTAAAIGTACATTTGAAAATTGTCAAGAAGCATTTTATAA---ACATCAATCTTTAA 385
                                                                                                                                                                                         355 AGAAACCCTACAAATGTGAAAGATGTGGAAAAGCCTTTAATCATTTCTCACACCTTACTA 414
                                                                                                                                                                                                                                                        GACATCATATATTATCTGTTCATGAAAAACATTAACGTGTAAACAATGTAATAAGTTT 445
                                                                                                                                                                                                                                                                                                                                                                                      446 TCACTCGACCTTCAAAATTAGCACAAACATAAAATTAAAACATCATGGTGGAATCTCCTGCTT 505
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                                                           295 gidgakakadceririkakceagrergekekeerrackekekekekekegakarrekekeegag 354
                                                                                                                                                                                                                                                                                                                       415 CACATAAGATAATTCATACTGGAGAGAACCTTACAAATGTAAAGRATGTGGTAAAGCTT 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                  475 TTAAACACTCTTCAACCTTACTAAACATAAGATAATTCATACTGGAGAGAAGCCTTACA 534
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 2694)

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Direct Submission
Submitted (01-FEB-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
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KEYWORDS
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NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs.remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, GA 94305
Web site: (Dickson, Mark) mcdepaxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1096
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1157 ACTACACATAAGTTCATCATGTTAAAGAAAAACCCTACAAATGT-----GAAGAATGT 1210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 AAAAAGTATATTGCACATATGAAGGGTGTGATAAAGCCTATAATCGACCATCATTATA 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Clone distribution: MGC clone distribution information can be four through the I.M.A.G.E. Consortium/LLML at: http://image.llnl.gov Series: IRAK Plate: 32 Row: f Column: 2 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein This clone has the following problem: frame shifted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 GAAAGTGACGAAACCAAATCGATATCATCTTTAATATCTTCTTCTTCTTCATCACGTCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue type="Brain, hypothalamus"
/clone lib="NIH MGC 96"
/lab host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4797857"
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Best Local Similarity 51.8
Matches 258; Conservative
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1216 gacaaagciririnaaccgarrcrcaraccrracraaacaraagaraarrcaricrggagag 1275
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2253)
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Submitted (08-AFR-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1042 GAATGTGGCAAAGCCTTCTACCATTCTTCACACCTTACTACAACATAAGGTAATTCATACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                307 CATGAAATCACCCATACAAAGTCATTTAAATGTACATTTGAAAATTGTCAAGAAGCATŢŢ
                                                                                                                                                                                                                                                                                    Length 2698;
                                                                                                                                                                                                                                                                                        7.3%; Score 90.4; DB 11; Length 51.8%; Pred. No. 4.1e-07; ive 0; Mismatches 231; Indels
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Contact: MGC help desk
Email: cgapbs-rammail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
/mol_type="mRNA"
/db_xref=".taxcn:9606"
/clone="IMAGE:4797729"
/tissue_type="Brain, hypothalamus"
/clone_lib="NHH MGC_96"
/lab_host="NHH MGC_96"
/note="NHOST"
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Mus musculus, clone IMACE:3674739, mRNA.
BC028252.1 GI:20380246
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                                                                                                                                                                                                                                                                                                                          Best Local Simi
Matches 258;
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I (basea 1 to 2698)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Schuler, G.B., Klausner, R.D., Collins, F.S., Wagner, L., Schemen, C.M., Schuler, G.D., Klausner, R.D., Collins, F.S., Wagner, L., Schemer, C.M., Schuler, G.D., Altschul, S.F., Jordan, H., Moore, T., Mars, S.I., Wang, J., Haich, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Staplecon, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninch, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., Malek, J.A., Gunzarne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, Y., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y. Butterfield, Y.S., Kazywinskin, I., Skalska, U., Smailus, D.E., Schein, J.E., Jones, S.J. and Marra, M.A., Schein, J.E., Jones, S.J. and Marra, M.A., Schein, J.E., Jones, S.J. and Marra, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLML at: http://image.llnl.gov estries: IRAK Plate: 70 Row: g Column: 16
This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not
                                                                                      BC037782 2698 bp mRNA linear HTC 19-NOV-2003 Homo sapiens hypothetical protein LOC148206, mRNA (cDNA clone INAGE:4797729), with apparent retained intron.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         info@bcgsc.bc.cd
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Letticia Hsiao, Martin Kzzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs.remail.nin.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (16-SEP-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
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This clone has the following problem: retained intron.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1, .2698
/organism="Homo sapiens"
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trausberg, R.
                                                                                                                                                                                                                                                                                               sapiens (human)
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PUBMED REFERENCE AUTHORS TITLE JOURNAL

FEATURES

JOURNAL MEDLINE

TITLE

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1. .604
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                                  g
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (INSC),
Gaithersburg, Maryland,
Web site: http://www.nisc.nih.gov/
Contact nisc.mgcmhpri.nih.gov/
Contact nisc.mgcmplyrinih.gov/
Akhter,N., Ayele,K., Beckerrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C.,
Dietrich,N.L., Granite,S., Gunn, X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogf,J.L., Malker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                           Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 65 Row: a Column: 17
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 13386417
This clone has the following problem: frame shifted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 CCCAAAAAGTATATTTGCACATATGAAGGGTGTGATAAAGCCTATAATCGACCATCATTA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITIATAAACA---TCAATCTTTAAGACATCATATATTATCTGTTCATGAAAAAACATTA 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124 TIAGAGCAACAITTAAGAACCCACAGTAATGATCGACCGTATAAATGTACAGTGGACGAT 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1177 TTTTCACAACACTTTCAACTCCAAAATCATATAAGAACACATACTAGAGAGATGCCTTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db xref="taxon:10090" /clone="IMAGE:3674739" /tissue_type="Wammary tumor metastatized to lung. Tuatose spontaneously from a senescent normal mammary clonal outgrowth infected with the virus MWTV." /clone_lib="NCI_CGAP_Lu29" /lab_host="DH10B"
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7.3%; Score 90.2; DB 11; Length 2253;
Best Local Similarity 51.9%; Pred. No. 4.6e-07;
Matches 256; Conservative 0; Mismatches 228; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/mol_type="mRNA"
/strain="CZECH II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAACATCATGGTG 493
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/note="Organ: head neck; Vector: pucl8; Site_l: Smal;
/note="Organ: head neck; Vector: Reverse transcription of tiesue mRNA and orbM amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Email: asimpsonalludwig.org.br
This asimpsonalludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=MR3-HT0446-260 300-201-f06&t13-200-03-26&t4=1)
Seq primer: puc 18 forward
High quality sequence stops: 583.
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21-JUN-2000
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EST 21-JUN-200
mRNA sequence.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69 AAAGTATATTTGGACATATGAAGGGTGTGAGTAAAGCCTAATAATGGACCATCATTATAGA
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          mRNA linear
Homo sapiens CDNA,
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larity 53.7%; Pred. No. 8.1e-07;
Conservative 0; Mismatches 193;
          604 bp
MR3-HT0446-260300-201-f06 HT0446
                                                                                                           BE161630
BE161630.1 GI:8624351
                                                                                                                                                                                                                                                                 Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                             BC032590 3609 bp mRNA linear HTC 19-NOV-2003 Homo sapiens cDNA clone IMAGE:5502691, containing frame-shift errors.
                                                                                                                                                                      515
ACCATICCATIGITCAGIGIGIGGIAAAAGGGGTTAATICICGACAACACTIGAAAAGACA 308
                      Accriacaacidiaangagigidecaagaccriigricaaaarrcarcrigiaargca 335
                                               TGAAATCACCCATAC -- AAAGTCATTTAAATGTACATTTGAAAATTGTCAAGAAGCATT 365
                                                                       TCACAAATCAAACCTTGCATGTCATCATAGACTTCATACTGGAGGAGAAACCTTACAAGTG 455
                                                                                                                                              TAAACAATGTAATAAAGTTTTCACTCGACCTTCAAAATTAGCACAACATAAAATTAAAACA 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (06-UN-2002) National Institutes of Health, Mammalian
Submitted (06-UN-2002) Cancer Genomics Office, National Cancer
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                           NIH-WGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: egapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
MNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
                                                                                                                                                                                                                                                                                                                      BC032590
BC032590.1 GI:21619671
                                                                                                                                                                                               486 TCATGGTGGATCTCCT 501
                                                                                                                                                                                                                        TATCGGAGAAAAACCT 531
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Homo sapiens
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                       276
                                                309
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MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
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AUTHORS
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COMMENT
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AL705393 535 bp mRNA linear EST 04-SEP-2003

DKFZp686M1835_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone

DKFZp686M1835_5', mRNA sequence.

AL705393.1 GI:19688748
Web site: http://www.nisc.nih.gov/
Contact: nites mgcMngri.nih.gov
Contact: nites mgcMngri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Grannite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Malker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,B.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: TRAK Plate: 69 Row: g Column: 20
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 13430873
This clone has the following problem: frame shifted.

1. 15699
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      249 ACCATTCCATTGTTCAGTGTGTGAAAGGGGTTAATTCTCGACAACACTTGAAAAGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAAGTATATTTGCACATATGAAGGGTGTGATAAAGCCTATAATCGACCATCATTATTAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  587 AGAGAAACCTTACAAATGTGAAGAATGTGACAAAGTTTTTAGTCGCTAATCACCTTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
7.2%; Score 89.2; DB 11; Length
Best Local Similarity 53.7%; Pred. No. 6.7e-07;
Matches 234; Conservative 0; Mismatches 193; Indels
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2004
Wed May 12 12:38:01
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This is the 5' sequence of the clone insert
This is the 5' sequence of the clone insert
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKF2): Email s.wiemann@dkfz-heidelberg.de;
sequenced by MediGenomix (Martinsried/Germany) within the cDNA
sequencing consortium of the German Genome Project. No sl sequence
available.
This clone (DKFZp686M1835) is available at the RZPD in Berlin.
Please contact the RZPD: Reseourcenzentrum, Heubnerweg 6, 14059
Berlin-Location/Qualifiers
1. 535
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Homora, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

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Ottenwaelder, B., Obermaier, B., Mewes, W., Mewes, H.W., Weil, B. and
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Unpublished (2001)
Contact: MIPS
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OS Candida albicans

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PD 24-SEP-2002

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PP 09-NOV-1999 UP 2005581204

PF 10-NOV-1999 UP 2005681204

PF 10-NOV-1999 PALLIER.SYLVIE CAMIER, ANDRE SENTENAC PC

C12N15/09,C12N15/09,A61K39/00,A61K45/00,A61F31/10,C07K14/40, PC

C12N15/09,C12N1/21,C12P21/02,C12Q1/02,G01N33/15,G01N33/50, PC

C12N11/19,C12N1/21,C12P21/02,C12Q1/02,G01N33/15,G01N33/50, PC

C12N15/00,C12R1:725)

C G10N33/53,

PC C12N15/00,C12R1:725)

C Candida albicans tfillAgene (CatfillA) and the coded CATFIIIA

CC Candida albicans tfillAgene (CatfillA) and the CODED CATFILLA

FT CDS

(12) . . (1235)

FT CDS
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; Pred. No. 1.7e-190;
0; Mismatches 0;

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forganism="Candida albicans"
/mol_type="genomic DNA"
/db_xref="texon:5476"

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Location/Qualifiers
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/organism='Candida albicans'
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            Location/Qualifiers
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/organism="Candida albicans"
/mol type="genomic DNA"
/db_xref="taxon:5476"
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1679 PAT 16-AUG-2002 ö 120 120 180 240 240 300 300 TTATTGGAGCAACATTTAAGAACCCACAGTAATGATCGACCGTATAAATGTACAGTGGAG 180 09 Candida albicans candida albicans saccharomycotina; Saccharomycetes; Bukaryota; Fungi; Ascomycota; Saccharomycetales; Candida. Saccharomycetales; mitosporic Saccharomycetales; Candida. ATAAAATCATTTACTGCTTCTTTGGAAGGTTCAAAAGGTGTTTCTAAAATCTTATTCTGAAT 1800 GATTTACGTCGACATTTGAAATGGCATGATGATAATTTACAAAGAATTGAGTCATTCTTA GATTGTGATAAAGCATTTTTCAGAAAATCACATTTGGAAACACATATTGTATCACATTCC 1740 AGTGGGAAGAAGATCAATTGTCCTAAGAATAATTGTGATAGAATGTTTTCTAGAGAATAT AATAGTATAGAAAAAAAAAAACTCCAGAAGGTGAACCATTGGTTAAAAAAGCCAGGATG TTATTAGAGCAACATTTAAGAACCCACAGTAATGATCGACCGTATAAATGTACAGTGGAC GATTGTGATAAAGCATTTTTCAGAAAATCACATTTGGAAAACACATATTGTATCACATTCC GAAAAAAAACCATTCCATTCAGTGTGTGTAAAGGGGTTAATTCTCGACAACACTTG GAAAAAAACCATTCCATTGTTCAGTGTGTGGTAAAGGGGTTAATTCTCGACAACACTTG ATAAAATCATTTACTGCTTCTTTGGAAGGTTCAAAGAGTGTTTCTAAACTTAATTCTGAAT AGTGGGAAGAAGATCTAATTGTCCTAAGAATAATTGTGATAGAATGTTTTCTAGAGAATAT GATTTACGTCGACATTTGAAATGGCATGATGATAATTTACAAAGAATTGAGTCATTCTTA <u> AATAGTATAGAAAAAGAAGAAGTCCAGAAGGTGAACCATTGGTTAAAAAAGCCAGGATG</u> ATGAGTGAAAGTGAAACCAAATCGATATCATCTTTAATATCTTCTTCTTCATCA <u>ATGAGTGAAAGTGAAACCAAATCGATATCATCTTTAATATCTTCTTCTTCATCA</u> CGTCCCAAAAAGTATTTGCACATATGAAGGGTGTGATAAAGCCTATAATCGACCATCA GATAGTCTAGATGAAAAAAAGAAGTGATGTTAGATCAGACTCAATGTCAGCTCAAAGATCA Gaps Roemer,T., Jiang,B., Boone,C., Bussey,H. and Ohlsen,K.L. Gene disruption methodologies for drug target discovery Patent: WO 02053728-A 6493 11-JUL-2002; Blitra Pharmaceuticals, Inc. (US) .; 0 Length 1239 Score 1235.8; DB 6; Length Pred. No. 5.4e-190; 0; Mismatches 2; Indels GATITATIGCCAAAIGAAACAICAGIGAITICICGAIAA 1239 1920 GATTTATTGCCAATGAACATCAGTGATTTCTCGATAA 1958 AX489193 1239 bp DNA Sequence 6493 from Patent WO02053728. AX489193 1. .1239 /organism="Candida albicans" /mol_type="unassigned DNA" /db_xref="taxon:5476"

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                     AAAAGACATGAAAATCACCCATACAAAGTCATTTAAATGTACATTTGAAAAATTGTCAAGAA
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AAAAGACATGAAATCACCCATACAAAGTCATTTAAATGTACATTTGAAAATTGTCAAGAA
                                                                    GCATTTTATAAACATCAATCTTTAAGACATCATATATTATCTGTTCATGAAAAACATTA
                                                                                                   361 GCATTTTATAACATCAATCTTTAAGACATCATATTATTATCTGTTCATGAAAAACATTA
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RESULT 4
YSCNOFEAT
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DEFINITION
Saccharomyces cerevisiae transcription factor IIIA and RNA
polymerase subunit RPB6 genes.
ACCESSION
M90638.1 GI:172046

2 965 ATGACGACTCACTAGTAACCAAAATTGGAAGTGTCATATATGTCCTGATATGTCTTTTT 1024 535 62 GTCCCAAAAAGTATTTGCACATATGAAGGGTGTGATAAAGCCTATAATCGACCATCAT 121 368 GGCCAAAGACATATTCTGTGACTATGATGGCTGTGATAAGGCATTTACAAGACCTTCAA 427 122 TATTAGAGCAACATTTAAGAACCCACAGTAATGATGACGGCGTATAAATGTACAGTGGACG 181 428 Tringacngaacaccaarraagcgracarcagggrrra---agaggarricagrgrgrafara 484 182 ATTGTGATAAAGCATTTTTCAGAAAATCACATTTGGAAACACATATTGTATCACATTCCG 241 485 AGTGTGCAAAATCCTTCGTTAAAAAGAGTCACTTAGAGAGACACTTGTATACGCATTCTG 544 301 545 ATACGAAACCATTCCAATGTTCTTATTGTGGAAAAGGAGTGACGACTCGCCAGCAACTGA 604 481 655 656 ATGATGATTCTACCATGATCAAAATATGGACTTGTGATTATTGTGATGTGGGGAAATTTG 715 302 AAAGACATGAAATCACCCATACAAAGTCATTTAAATGTACATTTGAAAATTGTCAAGAAG 361 605 AGCGACACGAAGTAACGCATACCAAATCTTTCATTTGTCCAGAAGGATGCAACCTCC 664 362 CATITITATAAACAICAATCTITAAGACAICATATATTATTTTGTTCATGAAAAAACATTAA 421 665 GATTCTACAAGCATCCACAATTAAGGGCACATATTTTATCTGTTCATTTACATAAACTAA 724 725 CCTGTCCACACTGCAATAAAAGCTTTCAGAGGCCATATAGGCTAAGAAATCACATTTCTA 784 785 AACATCACGATCCTGAGGTAGAAAATCCTTACCAATGTACTTTTGCTGGTTGTTGCAAAG 844 845 AGTITCGGATATGGICACAATIGCAATCGCATATAAAAAATGATCATCCTAAATTAAAAT 904 source text: Saccharomyces cerevisiae (strain S288C) DNA. Location/Qualifiers Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetaces; Saccharomycetaces; I (bases I to 150) Woychik, N.A. and Young, R.A. Genes encoding transcription factor IIIA and the RNA polymerase common subunit RPBG are divergently transcribed in Saccharomyces 482 AACATCA-----TGGTGGATCTCCTGCTTATCAATGTGATCATCCTGGTTGTTTAAAA 242 AAAAAAACCATTCCATTGTTCAGTGTGTGGGTAAAGGGGTTAATTCTCGACAACACTTGA CGTGTAAACAATGTAATAAAGTTTTCACTCGACCTTCAAAATTAGCACAACATAAATTAA 596 GTCCTAAATGTGGGTAAAGGTTGTGGGAAAAAAAGGTTTATCTTCACATATGTTAAGTC 536 ATTICCAAACTIGGICAGIATIACAATITICATATAAAACAACTGCATCCAAAACTTAAAI 905 GICCIATITGIAGCAAACCAIGIGIGGGGGAAAAIGGITTACAAAIGCACAIGAITATIC Match 17.5%; Score 217.4; DB 8; Length 1560; Local Similarity 59.4%; Pred. No. 1e-25; les 409; Conservative 0; Mismatches 271; Indels 9; cerevisiae Proc. Natl. Acad. Sci. U.S.A. 89 (9), 3999-4003 (1992) 92237295 /organism="Saccharomyces cerevisiae" /mol_type="genomic DNA" /strain="S288C" RNA polymerase, transcription factor IIIA. Saccharomyces cerevisiae (baker's yeast) Saccharomyces cerevisiae 1025 CTAGAAACATGATCTTCTCACGCATTAT 1053 CAAAGAAAATGAATTAGTTGAACATTAT 744 /db_xref="taxon:4932" chromosome 14. 1. .1560 Original 422 Query Match SOURCE source REFERENCE AUTHORS TITLE JOURNAL MEDLINE PUBMED Matches KEYWORDS FEATURES COMMENT ORIGIN dG à d 8 셤 8 ò g ò d ò 임 ò g ò 셤 ò 셤 ò 셤 à 엄 ઠ

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234. .1223

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/gene="TFIIIA"

/note="ainc finger containing protein"

/note="ainc finger containing protein"

/note="ainc finger containing protein"

/producE="transcription factor IIIA"

/producI="transcription factor IIIA"

/protein_id="AAS08014.1"

/protein_id="MAGRILANGHELAELKQETIPISRSESESINSLISTRSSSSN

/translation="WGGRAVTROQUERHEDVHENGHERPCONCAKSFVKKSHLERHLYTH

RPKTYPCDYDGCDKAPTRROQUERHEDVHTKSFICPESCONLRFYREPOLIANTH

RPKTYPCDYDGCDKAPTRROGUERHENTHISWHLSWHL

HTGEDIPELKYRTSDIQQLVQDHMIIHDDSLVTKWWKCHICDDMSFSRRHDLTHYGEI

HTGEDIPELKYRTSDIQQLVQDHGVQLQMSKHNBODEEKISNRLRKRKTFRNNNV

ETQNBVDLERKLESGENGLIALLLANTVGRKYRCFYNNCSRTFKTKERKTFRNNNV

ETKINILQEKEENKTILVDQNHKEPFIIQKETQSAGDK"
                                                      YSCTFIIIA 1739 bp DNA linear PLN 13-SEP-1996 Saccharomyces cerevisiae transcription factor IIIA (TFIIIA) gene, complete cds.
                                                                                                                               M80611.1 GI:172902

transcription factor IIIA; zinc-finger protein; zinc-finger
transcription factor.
Saccharomyces cerevisiae (baker's yeast)
Saccharomyces cerevisiae
Saccharomycetales; Saccharomycetina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomycete

1 (bases I to 1739)
Archambault, J., Milne, C.A., Schappert, K.T., Baum, B., Friesen, J.D.
and Segall, J.
The deduced sequence of the transcription factor TFIIIA from
Saccharomyces cerevisiae reveals extensive divergence from Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  242 AAAAAAACCATTCCATTGTTCAGTGTGTGAAAAGGGGTTAATTCTCGACAACACTTGA 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Saccharomyces cerevisiae"
/mol_type="genomic DNA"
/strain="%303-1A"
/db.xref="texon:4932"
/chromosome="XVI"
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J. Biol. Chem. 267 (5), 3282-3288 (1992)
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Saccharomyces cerevisiae (baker's yeast)

Baccharomyces cerevisiae

Eukaryotza; Fungi, Ascomycota; Saccharomycetes;

Bukaryotza; Fungi, Ascomycota; Saccharomycetes;

Saccharomycetales; Saccharomycetacee; Saccharomyces:

1 (bases 1 to 37497)

Saccharomyces, S. Brinkman, R., Cooper, J., Ding, H., Du, Z., Favello, A., Fulton, L., Gattung, S., Gatco, T., Kirsten, J., Kucaba, T., Hallsevth, K., Hawkins, J., Hilliet, L., Jier, M., Johnson, D., Johnston, L., Langston, Y., Latreille, P., Le, T., Mardis, E., Mardis, E., Wohldman, P., Vaudin, M., Wilson, R., Peluso, D., Rifken, L., Riles, L., Taich, A., Trevaskis, E., Vignati, D., Wilcox, L., Wohldman, P., Vaudin, M., Wilson, R. and Waterston, R.

In beginned of a portion of the right arm of Saccharomyces cerevisiae chromosome XVI

Unpublished (1995)
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                                                                                                                                                                                                                                                  482 AACATCA----TGGTGGATCTCCTGCTTATCAATGTGATCATCCTGGTTGTTTTAAAA 535
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                                                     664 GATICTACAAGCATCCACAATTAAGGGCACATATTTTATCTGTTCATTTACATAAACTAA
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CATITIATAAACATCAATCTTTAAGACATCATATTATCTGTTCATGAAAAAACATTAA
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This sequence includes nucleotides 1-37497 of cosmid 9677.
Cosmid on the left is 9705.
Location/Qualifiers
1. 37497
/ organism="Saccharomyces cerevisiae"
/mol_type="genomic DNA"
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Submitted (27-APR-1995) Robert Waterston
Submitted by:
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complement(16937, .19570)
/gene="P9677.13"
/gene="P9677.13"
/fore="P9677.13"
/note="Similar to S. cerevisiae hypothetical protein HRD799 (PIR accession number $45161) and S. pombe
                                                                                                                                                                                                                                                                        9; Gaps
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YSCRP026A 2133 bp DNA linear PLN 27-APR-1993 S.cerevisiae RNA polymerase II sixth subunit (RP026) gene, complete M33924

RESULT 7 YSCRP026A/c DEFINITION ACCESSION

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                                                                                                        Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetes; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomyces.

1 (bases 1 to 2133)
Archambault,J., Schappert,K.T. and Friesen,J.D.
A suppressor of an RNA polymerase II mutation of Saccharomyces
cerevisiae encodes a subunit common to RNA polymerases I, II, an
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RNA polymerase II, c-myc proto-oncogene, transmembrane protein;
tyrosine kinase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .2133
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join[1026. 1045,1122. .1569)
/note="RNA polymerase II sixth subunit (RP026)"
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/note="RR026 intron A"
1022 ...1569
/note="RNA polymerase II sixth subunit (RP026)
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Pred. No. 8.2e-23;
0; Mismatches 208;
                                                                                                                                                                                                                                                                                                                  . Cell. Biol. 10 (12), 6123-6131 (1990)
                                                       Saccharomyces cerevisiae (baker's yeast)
Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Draft entry and computer-readable seque kindly submitted by J.D. Friesen, 101-MAY-1990.

by J.D. Friesen, 101-MAY-1990.

The Hospital for Sick Children 555 University Avenue Toronto, Ontario, CANADA M5G 1X8 e-mail: jim@sickkids.toronto.edu. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
/protein_id="AAA34989.1"
/db_xref="G1:172453"
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llarity 61.4%;
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Direct Submission

Submitted (07-5EP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail:
seqref@genoscope.orns.fr - Web: www.genoscope.cns.fr)
This STS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus war. uvarum, Saccharomyces
exiguus, Saccharomyces bayanus war. uvarum, Saccharomyces
lactis var. lactis, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus pichia
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UNSUGING 797 bp DNA linear STS 30-NOV-2001 T7 end of clone ASOAA022B07 of library ASOAA from strain CLIB 533 of Saccharomyces bayanus, sequence tagged site.
256 TCACATTTCTAAACATCACGATCCTGAGGTAGAAAATCCTTACCAATGTACTTTTGCTGG 197
                                                                TIGITITAAAAATTTCCAAACTTGGTCAGTATTACAATTTCATATAAAACAACTGCATCC 584
                                                                                                                              trorrecaaagarrregarargareacaarrecaareecararaaaaarearearee 137
                                                                                                                                                                                           585 AAAACTTAAATGTCCTAAATGTGGTAAAGGTTGTGGGAAAAAAAGGTTTATCTTCACA 644
                                                                                                                                                                                                                                                                                                                                645 TAIGTTAAGTCATGATGATTCTACCATGATCAAAATATGGGACTTGTGATTATTGTGATGT 704
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Fung; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomyces.

(bases 1 to 797)
Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G.,
Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,
Antigny, J., Dujon, B., Durrens, P., Lepingle, A., Liorente, B.,
Malbertuy, A., Neuvelise, C., Ozier-Kalogeropoulos, O., Potier, S.,
Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
Wincker, P. and Weissenbach, J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bon, E., Neuveglise, C., Casaregola, S., Artiguenave, F., Wincker, P., Aigle, M. and Durrens, P.
                                                                                                                                                                                                                                                               136 TAAATTAAAATGTCCTATTTGTAGCAAACCATGTGTGGGGGGAAAATGGTTTACAAATGCA
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/clone=lib="ASQAA"
/clone=lib="ASQAA"
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/evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                              83 GACAATTGTGCAAAATCCTTTGTTAARAAGAGTCATCTAGAGAGGCACTTGTTTTCGCAT 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   238 TCCGAAAAAAACCATTCCATTGTTCAGTGTGTGTAAAGGGGTTAATTCTCGACAACAC 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  143 TCTGATACGAAGCCATTCCAATGTTCTTATTGTGGCAAGGGGGTGACAACTCGACAGCAA 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 478 TTAAAACATCATGGT-----GGATCTCCTGCTTATCAATGTGATCATCGGTTGTTTT 531
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DOE Joint Genome Institute and Stanford Human Genome Center.
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Homo sapiens chromosome 19 clone RP11-274A19, complete sequence.
AC138126
AC138126.1 G1:27151357
HTG.
                                                                                                                                                                                                                                                                                                                                                               178 GACGATTGTGATAAAGCATTTTTCAGAAAATCACATTTGGAAACACATATTGTATCACAT
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DOE Joint Genome Institute and Stanford Human Genome Center.
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                                                                                                                                                                                                                                                             Query Match 15.6*; Score 193; DB 11; Length 75 Bet Local Similarity 59.3*; Pred. No. 15-21; Matches 347; Conservative 1; Mismatches 231; Indels.
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Direct Submission
Submitted (19-UNA-2002) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Jun 19, 2002 this sequence version replaced gi:13699752.
Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                        Direct Submission
Submitted (22-JJM-2000) Production Sequencing Facility, DOE Joi
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598,
3 (bases 1 to 177299)
1 (bases 1 to 177299)
DOB Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                         www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www.shor.stanford.edu
www.shor.stanford.edu
Guality: Phraz Quality >=40 99.9% of Sequence;
Estimated Total Number of Errors is 0.2.
NOTE: BACTERIAL TRANSPOSONS excised at 14620 and 98099.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .177299
/organism="Homo sapiens"
/or Lype="genomic DNA"
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                                                                                                    2 (bases 1 to 177299)
DOE Joint Genome Institute.
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     Submitted (17-DEC-2002) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA Drift Sequence Produced by DOB Joint Genome Institute www.joi.doe.gov Pinishing Completed at Stanford Human Genome Center www.shgo:stanford.edu Quality: Phrap Quality >=40 100% of Sequence; Estimated Total Number of Errors is 0.
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50.9%; Pred. No. 2e-07;
tive 0; Mismatches 280; Indels
                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/mol_type="genomic DNA"
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/mol_xref="taxon:9606"
/chromosome="19"
/clone="RP11-274A19"
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Matches 298; Conservative
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  8.2%; Score 101; DB 9; Length 17
50.8%; Pred. No. 2e-07;
iive 0; Mismatches 280; Indels
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AC073544 177299 bp DNA linear PRI 19-JUN-2002 Homo sapiens chromosome 19 clone RP11-359H1B, complete sequence.

AC073544 AC073544.4 GI:21465367 Homo sapiens (human)

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

RESULT 10 AC073544/c LOCUS

DEFINITION

Homo sapiens Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

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Homo sapiens
similar to Z1
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Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R.,
Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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163206 ACTTGATTGTGCATAAGATAATTCATACTAAAAAAAAACCTACAAGT 163160
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Full-1679th cDNAs
Patent: BP 1293569-A 726 19-MAR-2003;
Helix Research Institute (JP); Research Association:
Biotechnology (JP)
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Seguence 726 from Patent EP1293569.
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Isogai,T., Otsuki,T. and Sugiyama,T.
Isogai,T., Otsuki,T. and Sugiyama,T.
Direct Submission
Submitted (24-OCT-2001) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Rax:81-438-52-3966)
NEDO human DNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; CDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA full insert sequencing:
Construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: RAB and
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mRNA linear PRI 01-AUG-2002
clone NT2RI2000341, moderately
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ninomiya, K., Wagatsuma, M., Kanda, K., Kondo, H., Yokoi, T.,
Kodaira, H., Furuya, T., Takahashi, M., Kikkawa, E., Omura, Y., Abe, K.,
Kamihara, K., Katsuta, N., Sato, K., Tanikawa, M., Yamazaki, IM.,
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Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S.,
Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T.,
Nabo human cDNA sequencing project
                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Pred. No. 1e-06;
); Mismatches 281;
                                                                                                                                                              AKO56088
AKO56088.1 GI:16551397
AKO56088.1 GI:16551397
Homo saping, fis (full insert sequence).
Homo sapiens (human)
Homo sapiens
     2132 bp
Siens cDNA FLJ31526 fis, cl
to ZINC FINGER PROTEIN 43.
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llarity 50.6%;
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us-09-831-804-2.rge

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Homo sapiens chromosome 19 clone RP11-189C24, *** SEQUENCING IN PROGRESS ***, 5 ordered pieces. AC138469 AC138469. I GI:27544967 HTG; HTGS PHASE2; HTGS ACTIVEFIN. Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAATGIGGCAAAGCITITAACCAGICCICAAICCITACIACACAIAAGAGAAITCAIACI 48640
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Estimated Total Number of Errors is 0.1.

NOTE: This insert is not the entire sequence of the clone (entire sequence is 153.9kb). It clipped at the overlap with AC008981. The number of bases overlapped is 27192.

Location/Qualifiers
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1 (Dases 1 to 169500)

DOE Joint Genome Institute and Stanford Human Genome Center.

Direct Submission
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297; Conservative
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Homo sapiens chromosome 19 clone RP11-209J6, complete sequence.
AC099500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (29-MXY-2002) DOE Joint Genome Institute, 2800 Mitchell
Submitted (29-MXY-2002) DOE Joint Genome Institute, 2800 Mitchell
Draft Sequence Produced by DOE Joint Genome Institute
Www.igi.doe.gov
Frinishing Completed at Stanford Human Genome Center
Www-shg: stanford.edu
Quality: Phrap Quality >=40 100% of Sequence;
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Catarrhini, Hominidae, Homo.
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                                                                                                                                                     1618 AAACCCTACCAATGTGAAGAATGTGGTAAAGCCTTTAACCAGTCCTCACACTTACTAGA
                                                                          1384 GAATGTGGCAAAGCTTTTAACCAGTCCTCAATCCTTACTACACATAAGAGAATTCATACT
                                                                                                                           67 AAAAAGTATATTTGCACATATGAAGGGTGTGATAAAGCCTATAATCGACCATCATTATTA
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                            7 GAPAGIGACGAAACCAAATCGATATCATCTTTAATATCTTCTTCTTCTTCATCACGTCCC
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1 (bases 1 to 138627)
DOB Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
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Direct Submission
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Unpublished

E (bases 1 to 169500)

S DOE Joint Genome Institute and Stanford Human Genome Center.

Direct Submission

Submitted (108-JAN-2003) DOE Joint Genome Institute, 2800 Mitchell

Drive, Walnut Creek, CA 94596, USA

* NOTE: This is a "working draft," sequence. It currently

* consists of 5 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be preserved.

* This sequence will be preserved.

* This sequence will be preserved.

* This sequence will be preserved.

* This sequence will be preserved.

* This sequence will be preserved.

* 1 75797 75895 contig of 62175 bp in length

* 138072 138171 gap of unknown length

* 157900 157999; gap of unknown length

* 157800 166058; contig of 8059 bp in length

* 166059 166158; gap of unknown length

* 166059 166158; gap of unknown length

* 166059 166158; gap of unknown length

* 166059 166158; gap of unknown length

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Best Local Similarity 50.6%; Pred. No. 3.7e-07;
Matches 297; Conservative 0; Mismatches 281; Indels 9; Gaps
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Center Code: JGI
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Center Project Name: 479013
Center clone name: RP11-189C24
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/organism="Homo sapiens"
/mol_type="genomic DNA"
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/chromosome="19"
/clone="RP11-189C24"
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RS Tanigami, A., Fujiwara, T., Shibahara, T., Goto, Y., Hirao, M., Shimizu, F., Wakebe, H., Ono, T., Hishigaki, H., Watanabe, T., Ozaki, K., Shimizu, F., Wakebe, H., Ono, T., Hishigaki, H., Watanabe, T., Ozaki, K., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamasu, A., Ishii, S., Yamashita, H., Maral, Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yanda, K., Wagatsuma, M., Murakawa, K., Kanda, M., Kanda, K., Magatsuma, M., Murakawa, K., Kandano, I., Sugano, S., Magatari, K., Mashino, Y., Nagai, K. and Isogai, T. NEDO human cDNA sequencing project Gai, K., And Isogai, T. and Yamamoto, J. (Lases 1 to 2237)

RS Isogai, T. and Yamamoto, J. (Chases 1 to 2237)

RS Isogai, T. and Yamamoto, J. (Chase 1 to 2237)

RS Isogai, T. and Yamamoto, J. (Chase 1 to 2237)

RS Isogai, T. and Yamamoto, J. (Chase 1 to 2237)

RS Isogai, T. and Yamamoto, J. (Chase 1 to 2237)

RS Isogai, T. and Yamamoto, J. (Chase 1 to 2237)

RS Isogai, T. and Yamamoto, J. (Chase 1 to 2237)

RS Isogai, T. and Yamamoto, J. (Chase 1 to 2237)

RS Isogai, T. and Yamamoto, J. (Chase 1 to 2237)

RS Isogai, T. and Yamamoto, J. (Chase 1 to 2237)

RS Isogai, T. and Yamamoto, J. (Chase 2 to 22-3986)

RS Isogai, T. and Yamamoto, J. (Chase 2 to 37)

Razusa-Kamatari, Kisarazu, Chiba 292-0818, Japan

RS Isogai, T. and Yamanoto, J. (Chase 2 to 37)

RESEARCH Association for Blotochology (RAB); chan library of Construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB; annotation: HRI and RAB.

RAB; annotation: HRI and RAB.

I Coally Chase Sequencing Profession (Technology and RAB) annotation: HRI and RAB.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                           49433 AAACCTACCAATGTGAAGAATGTGGTAAAGCCTTTAACCAGTCCTCACACCTTACTAGA
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                                                                                                                                        CATGAAATCACCCATACAAAGTCATTAAATGTACATTTGAAAATTGTCAAGAAGCATTT
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2237 bp mRNA linear PRI 09-SEP-Homo sapiens cDNA FLJ16502 fis, clone FEBRA2006664, moderately similar to Zinc finger protein 43.
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AK122869.1 GI:34528067
oligo capping; fis (full insert sequence).
Homo sapiens (human)
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247
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2066 TGCTGGTGAGAAATCTTAGAATGTGAAGATGTAACAAAACCTTTAAAAGTTGTACAC 2128
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Query Match 7.9%; Score 98.2; DB 9; Length 2237; Best Local Similarity 52.0%; Pred. No. 1.6e-06; Matches 273; Conservative 0; Mismatches 243; Indels 9;
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Search completed: May 9, 2004, 08:56:51 Job time : 5094.16 secs

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May 9, 2004, 03:47:06; Search time 545.661 Seconds (without alignments) 9646.138 Million cell updates/sec
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1239
1 atgagtgaaagtgacgaaac......catcagtgatttctcgataa 1239
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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1: __geneseq11980s; *

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

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	XX	Transcription factor; CATFILIA; DNA-binding protein; ribosomal RNA 5S gene; fungal infection; ss. Candida albicans. Key 100cation/Qualifiers CDS 720. 1958 *tag= a *tag= a /transl_except= (pos: 1296. 1298, aa: /transl_except= (pos: 1734. 1736, aa: /transl_except= (pos: 1734. 1736, aa:	DNA encoding a transcription factor designated CATFILIA Transcription factor; CATFILIA; DNA-binding protein; ribosomal RNA 5S gene; fungal infection; ss. Candida albicans. Key Too: 1958 /*tag= a //transl_except= (pos: 12961298, aa: //transl_except= (pos: 17341736, aa:	AAA15398; 04-SEP-2000 (first entry) DNA encoding a transcription factor designated CATFILIA Transcription factor; CATFILIA; DNA-binding protein; ribosomal RNA 5S gene; fungal infection; ss. Candida albicans. Key 720. 1958 720. 1958 720. 1958 720. 1988 as: /tanal except= (pos: 1296. 1298, aa: /transl_except= (pos: 1734. 1736, aa:
		Transcription factor; CATFIIIA; DNA-binding ribosomal RNA 5S gene; fungal infection; 88. Candida albicans.	DNA encoding Transcription ribosomal RNA Candida albic	AAA15398; 04-SEP-2000 DNA encoding Transcription ribosomal RNP Candida albic

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protective against fungal infection and to raise antibodies. Such antibodies, as well as the polypeptides and polymuclectides are used in compositions for diagnosing and treating fungal infections, e.g. by detecting polymorphisms and mutations
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                                                                                                                                                      Length 2060;
                                                                                                          Sequence 2060 BP; 726 A; 315 C; 354 G; 665 T; 0 U; 0 Other;
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                                                                                                                                                    100.0%; Score 1239; DB 3;
100.0%; Pred. No. 2.5e-234;
ive 0; Mismatches 0;
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Matches 1239; Conservative
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1620 GATAGTCTAGATGAAAAAAAGAGGTGATGTTAGATCAGACTCAATGTCAGCTCAAAGATCA 1679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to constructing (M1) a strain of diploid fungal cells in which both alleles of a gene are modified, comprising modifying one allele by insertion or replacement by a cassette having an expressible selectable marker and modifying other allele by recombination, of a promoter replacement fragment with a heterologous promoter, so that expression of the second allele is regulated by the promoter. (M1) is useful for constructing a strain of diploid fungal cells in which both alleles of a gene are modified. The diploid fungal cells having both alleles modified are useful for identifying a gene that is essential to the survival or growth of a fungus, a gene that contributes to the virulence and/or pathogenicity of a fungus, a gene
                                                                                                                                           1680 ATAAAATCATTTACTGCTTCTTTGGAAGGTTCAAAGAGTGTTTCTAAACTTATTCTGAAT
                                                                                                                                                                                                                                                                                                       1740 AGTGGGAAGAAGATCAATTGTCCTAAGAATAATTGTGATAGAATGTTTTCTAGAGAATAT
                                                                                                                                                                                                                               1021 AGTGGGAAGAAGATCAATTGTCCTAAGAATAATTGTGATAGAATGTTTTCTAGAGAATAT
                                                                           ATAAAATCATTTACTGCTTCTTTGGAAGGTTCAAAGAGTGTTTTCTAAACTTATTCTGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fungus; yeast, tetracyclin, promoter; GRACE strain, biosynthesis; signal transduction, DNA replication, cell division; growth; proliferation; Candida albicans; fungicide; antifungal; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 37; SEQ ID NO 6493; 167pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1201 GATTTATTGCCAAATGAAACATCAGTGATTTCTCGATAA 1239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Candida albicans essential gene SEQ ID NO 6493.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABZ32206 standard; DNA; 1239 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Boone C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-DEC-2000; 2000US-0259128P.
20-FEB-2001; 2001US-00792024.
22-AUG-2001; 2001US-0314050P.
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that contributes to the resistance of a diploid fungus to an antifungal agent, an antifungal agent that inhibits the growth of a diploid fungus and for identifying a therapeutic agent for treatment of a mammalian disease. (MI) is useful for identifying a compound which modulates the activity of a gene product, preferably ensymatic activity, carbon compound catabolism, biosynthetic, transporter, transcriptional, translational, asgnal transduction, DNA replication and cell division activity. The method is useful for identifying a compound having the ability to inhibit growth or proliferation of C. albicans cells and for treating infection by C. albicans. The present sequence is that of an essential Candida albicans gene used in the method of the invention. Note: The sequence date for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office
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Seguence 1239 BP: 481 A: 171 C: 215 G: 372 T: 0 U: 0 Other:

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Sequence 1239 BP; 481 A; 171 C; 215 G; 372 T; 0 . Ty Match 99.7%; Score 1235.8; DB 6	11 Similaricy 99.84; Freq. NO. 9.86-234; [237; Conservative 0; Mismatches 2; I	a ggaaa ccaaatggatatcatctttaatatcttcttct 	61 CGTCCCAAAAAGTATATTIGCACATATGAAGGGTGTGATAAAGCCTATAATGGACCATCA 	121 TTATTAGAGCAACATTAAGAACCCACAGTAATGATCGACCGTATAAATGTACAGTGGAC 	181 GATTGTGATAAAGCATTTTGAGAAATCACATTTGGAAACACATATTGTATCACATTCC 	241 GAAAAAAACCATTCCATTGTTCAGGGGGGGAAAAGGGGTTAATTCTCGACAACACTTG 	301 AAAAGACATGAAATGACCCATACAAAGTCATTTAAATGTACATTTGAAAATTGTCAAGAA 	361 GCATTTTATAAACATCAATCTTTAAGACATGATATATTATCTGTTCATGAAAAAACATTA 	421 ACGIGTAAACAATGTAATAAAGTTTTCACTGGACCTTCAAAATTAGGACAACATAAATTA (1)	481 AAACAICATGGIGGAICTCCTGCTTAICAATGIGATCAICCTGGITGTITTAAAAITTC	541 CAAACTTGGTCAGTATTACAATTTCATATAAAACAACTGCATCCAAAACTTAAATGTCCT 	601 AAATGTGGTAAAGGTTGTGTTGGGAAAAAAGGTTTATCTTCACATATGTTAAGTCATGAT 601 AAATGTGGTAAAGGTTGTGTGGGAAAAAAGGTTTATCTTCACATATGTTAAGTCATGAT	661 GAITCIACCAIGATCAAAATAIGGACTIGIGATTAIIGIGAIGIGGGGAAAITIGCAAAG 	721 AAAAATGAATTAGTTGAACATTATAATATCTTCCATGATGGTAATATCCTGATGATTTA 721 AAAAATGAATTAGTTGAACATTATAATATCTTCCATGATGGTAATATCCCTGATGATTA

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<u>අ</u> ධ	781	
ò	841	aattigcatgaattagaaacagagaaattaaaagtggaagaagatgaagaagatgaagaa
<u>අ</u> ධි	841	
ð 6	106	GATAGTCTAGATGAAAAAGAAGTGATGTTAGATCAGACTCAATGTCAGCTCAAAGATCA 960 GATAGTGTAGATGAAAAAAAAAAAAAAAAAAAAAAAAA
3	100	
ò f	196	ATAAANCATTTACTGCTTCTTTGGAAGGTTCAAAGAGTTTCTAAACTTTATTCTGAAT 102 ####################################
ar —	1 o h	AIAAAAICAITIACIGCIICIIIGGAAGGIICAAAGAGIGIIICIAAACIIAIICIGAAT 102
ð f	1021	AGTGGGAAGAAGATCAATTGTCCTAAGAATAATTGTGATAGAATGTTTTCTAGAGAATAT 1080
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∂ :	1801	GATI IACGICOACATI IOANAL GGCATOA I TACAAAAAAA I GAGICATI CITA
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RES ADA		8 standard Olso BD
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XX XX	ADASAISB	
123	N	003 (first entry)
\$ E \$	Human coding	ding sequence, SEQ ID 726.
₹ ₹	Cytostat	Noot:
₹ <u>₹</u> ₹	Gene The	: Therapy; human; secretory protein; memorane proteins; cancer; ammatory disease; osteoporosis; neurological disease; gene; ss.
Sos	Homo sapi	ens
- A	9	9-82.
\$ B !	19-MAR-200	003.
¥ & \$	C/4	002; 2002EP-00006586
PR	$\alpha \alpha$	001; 2001JP-00328381. 002; 2002US-0350435P.
XX AP	(HELI-) (REAS-)	HELIX RES INST. RES ASSOC BIOTECHNOLOGY.
XX PI PII	XX PI Isogai T PI Yamamoto PI Seki N,	T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S; o J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I; Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
X & & ;	WPI; 200 P-PSDB;	003-395539/38. ; ADAS4797.
XX TY TY	New poly and/or m which th	New polynuclectides encoding full-length polypeptides, e.g. secretory and/or membrane proteins, useful for developing medicines for diseases in which the gene is involved, or as target molecules for gene therapy.
XX S	Claim 1;	SEQ ID NO 726; 205pp; English.

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1678 CATAAGAGAATTCATACTGGAGAGAACCCTACCAATGTGAAAAATGTGGGAAAGCTTTT 1737
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                                                                                                                                                                                                                                                                                                                   9; Gaps
                  The present invention relates to novel human secretory or membrane proceins (ADA54072-ADA55710) and their coding sequences (ADA52433-ADA54071). The coding sequences are useful in the gene therapy of diseases caused by abnormalities of the proteins, e.g. cancer, inflammatory diseases, osteoporosis or neurological disease.
                                                                                                                                                                                                                                                      8.0%; Score 99.4; DB 7; Length 2132; 0.6%; Pred. No. 3.3e-10; ve 0; Mismatches 281; Indels 9.
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                                                                                                                                                                                                 Seguence 2132 BP; 833 A; 423 C; 347 G; 529 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                 50.6%;
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Matches 297; Conservative
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Human, nucleic acid-associated protein, cytostatic; antiarteriosclerotic; anticonvulsant; nootropic; neuroprotective; cerebroprotective; anti-HIV; antionflergic; antiinflammatory; thyromimetic; gene therapy; cell proliferative disorder; cancer; atherosclerosis; neurological disorder; epilepsy; Huntington's disease; stroke; immune disorder; inflammatory disorder; AIDS; allergy; protein-protein interaction; Hypothyroidism; Cushing's syndrome; infection; gene expression profile; gene; ss.
                                                                                                                                                                                                                             cDNA encoding human nucleic acid-associated protein (NAAP) #51.
ACA98970 standard; cDNA; 1705 BP
                                                                                                                                                                                       25-JUL-2003 (first entry)
                                                                                  ACA98970
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The invention describes a novel human isolated mucleic acid-associated diagnosing, tracting and preventing diseases or conditions associated diagnosing, tracting and preventing diseases or conditions associated with the decreased expression or vorsexpression of NAAP, such as cell proliferative (e.g. cancer, atherosolerosis), neurological (e.g. appliepsy, Huntington's disease, stroke), immune/inflammatory (e.g. AIDS, allergies) and developmental (e.g. Hypothyroidism, Cushing's syndrome) disorders, or infections. These are also useful in assessing the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of NAAP. The NAAP or its fragments are useful in screening compounds for effectiveness as agonist or antegonist of the polypeptides, or in altering the expression of the target polymucleotide and compounds that specifically bind to or modulate the activity of the polypeptide. The specifically bind to or modulate the activity of the polypeptide. The account of the carrier of the polypeptide. This sequence encodes a novel human nucleic acid-associated protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New human nucleic acid associated proteins (NAAP), useful for diagnosing, treating and preventing diseases or conditions associated with the aberrant NAAP expression e.g. cancer, AIDS, atherosclerosis, epilepsy, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 AAAAAGTATATTTGCACATATGAAGGGTGTGATAAAGCCTATAATCGACCATCATTATTA 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Tang YT, Jackson JL, Griffin JA, Elliott VS, Forsythe IJ;
Becha SD, Richardson TW, Lee EA, Sprague WW, Emerling BM;
Thangavelu K, Warren BA, Tran UK, Yue H, Xu Y, Yue H, Li JX;
Hafalia AJA, Sanjanwala B, Marquis JP, Gorvad AE, Lee SY, Ison CH;
Baughn MR, Chawla NK, Nguyen DB, Swarnakar A, Zebarjadian Y, Shah
Thornton M, Yao MG, Khan FA, Gandhi AR, Yang J, Kable AE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1705 BP; 622 A; 305 C; 314 G; 464 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 5; Page 340-341; 345pp; English.
                                                                                                                                                                                         07-SEP-2001; 2001US-0317792P.
07-SEP-2001; 2001US-0317912P.
14-SEP-2001; 2001US-0322270P.
28-SEP-2001; 2001US-0326732P.
19-0CT-2001; 2001US-0346716P.
25-JAN-2002; 2002US-0351749P.
22-FEB-2002; 2002US-0351749P.
                                                                                                                                                       05-SEP-2002; 2002WO-US028540
                                                                                                                                                                                                                                                                                                                                                                                                      (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Burford N, Ramkumar J;
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                                                               WO2003023003-A2
                        Homo sapiens.
                                                                                                           20-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1049 AACCAAGCCTCAAAGCTTACTGAACATAAGTTAATTCATACCGGAGAGAAATGCTACAAA 1108
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                                                               928
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signalling pathway population; cancer; adenocarcinoma; leukaemia;
immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.
                                                               GGCAAAGCCTTTAACCAGACCTCACACCTTATTAGACATAAGAGAATTCATACTGAAGAG
                                                                                                                                                                                                                                                                                                                                             989 CATAATATATATCATACTGGGGAAATTCCCTACAAATGTGAGAAATGTGTTAGAGCTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                    367 TATAAACATCAATCTTTAAGACATCATATATTATCTGTT---CATGAAAAACATTAACG
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GATAAAGCATTTTTCAGAAAATCACATTTGGAAACACACATATTGTATCACATTCCGAAAAA
                                                                                                                                      AAACCATTCCATTGTTCAGTGTGTAAAGGGGTTAATTCTCGACAACACTTGAAAGA
                                                                                                                                                                                                      929 AAACCCTACAAATGTGAAGAATGTGGCAAAGCCTTTAACCAGTCATCGACCTTACTACA
                                                                                                                                                                                                                                                                             CATGAAATCACCCATACAAAGTCATTTAAATGTACATTTGAAAATTGTCAAGAAGCATTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human signalling pathway polynucleotide probe SEQ ID NO 1054.
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combination is also useful for purifying a subpopulation of mRNAs, cDNAs and genomic fragments and in research and diagnostic applications. The array can detect changes in expression in a large number of genes coding for different saymaling pathway populations which can be used to diagnose various diseases including cancer e.g. adenocarcinoma and leukaemia, immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzhelmer's disease and Parkinson's disease. The present sequence represents a polymucleotide probe of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at
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7.8%; Score 96.6; DB 7; Length 2320;
Best Local Similarity 51.3%; Pred. No. 1.2e-09;
Matches 306; Conservative 0; Mismatches 279; Indels 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2320 BP; 903 A; 423 C; 412 G; 582 T; 0 U; 0 Other;
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1609 CATAAGATAATTCATACTGGAAAGAAACCCTACAAATGTGAAGAAGAAGGAAAGCTTTT
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2001US-0301787P.
2001US-0301792P.
2001US-0301892P.
2001US-0303443P.
2001US-0303443P.
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P-PSDB; AAO16419.
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Richardson TW,
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Arvizu CS, I
Ramkumar J,
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15-MAR-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated polynuclectide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
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                                                                                                                                                                                                                        2000US-00540217
2000US-00649167
                                                                                                                                                                   2001WO-US008631
                                                                                                                                                                                                                                                                                                                                                                                                                          WFI; 2001-639362/73.
P-PSDB; ABG27130.
                                                                                                                                                                                                                                                                                                                                                                         Liu C,
                                                                                                                                                                                                                                                                                                              (HYSE-) HYSEQ INC
                                                    WO200175067-A2
                                                                                                                                                                                                                        31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                30-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                      Drmanac RT,
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                                                                                                        11-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, gene; ds; nucleic acid-associated protein, NAAP; arteriosclerosis; cell proliferative disorder; atherosclerosis; cirrhosis; hepatitis; AIDS; cancer; developmental disorder; renal tubular acidosis; anaemia; asthmä; mental retardation; neurological disorder; Alzheimer's disease; epilepsy; Parkinson's disease; autoimmune disorder; inflammatory disorder; allergy; Crohn's disease; transgenic animal; animal model.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SY;
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Y;
TAIDAACATCAATCTTTAAGA---CATCATATATTATCTGTTCATGAAAAACATTAAGG
                                                                                   1669 AGCCAGTCCTCAACCTTAGAAACCATCAGATAATTCATACTGGAGAGAAACCCTACAAA
                                                                                                                                                                                      424 TGTAAACAATGTAATAAAGTTTTCACTCGACCTTCAAAATTAGCACAACATAAATTAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human nucleic acid-associated protein coding sequence - SEQ ID No 52.
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New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess

Claim 1; SEQ ID NO 390; 103pp; English.

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1183
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or cancer); developmental disorders (e.g. renal tubular acidosis, anaemia or mental retardation); neurological disorders (e.g. Alzheimer's disease, Parkinson's disease or epilepsy); and autoimmune/inflammatory disorders (e.g. AlbS, allergies, asthma or Crohn's disease). The DNA sequences of the invention are useful for creating transgenic animals to model human disease. The present DNA sequence encodes a human nucleic acid-associated protein of the invention
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                                                                                                                                                                                                                                    78 TIGCACATATGAAGGGIGIGATAAAGCCTATAATCGACCATCATTATAGAGCAACATTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  375 TCAATCTTTAAGACATCATATATTATCTGTTCATGAAAAAACATTAACGTGTAAAAATG
                                                                                                                                                                                                                                                                                                  138 AAGAACCCACAGTAATGATCGACCGTATAAATGTACAGTGGACGATTGTGATAAAGCATT
                                                                                                                                                                                                                                                                                                                                   1130 GAGAÁTTCÁTACTGGAGAGAAACCTTACAAATGT-----GAAGÁGTGTGGGAAAGCCTT
                                                                                                                                                                                                                                                                                                                                                                   Gaps
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medical imaging; diagnostic; genetic disorder;
                                                                                                                                                                                                    ω.
                                                                                                                                                                     Length 2597;
                                                                                                                                    Sequence 2597 BP; 947 A; 504 C; 505 G; 641 T; 0 U; 0 Other;
                                                                                                                                                                   Score 94.6; DB 7; Length 2
Pred. No. 3e-09;
0; Mismatches 179; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    novel human diagnostic protein #390.
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                                                                                                                                                                     7.6%;
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                                                                                                                                                                                     Local Similarity 55.1
nes 231; Conservative
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                                                                                                                                                                                                                                                                                                                                                                     198
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of altes expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and amin a cid sequences. AASA64 represent nowel human diagnostic and to produce other types of AASA9464 represent nowel human diagnostic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   189 TAAAGCATTTTTCAGAAAATCACATTTTGGAAACACATATTGTATCACATTCCGAAAAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                191; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.5%; Score 92.4; DB 5;
llarity 54.1%; Pred. No. 8.6e-09;
Conservative 0; Mismatches 191;
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nes 236; Conserva
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Liu C,

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Drmanac

(HYSE-) HYSEQ INC

WPI; 2001-639362/73

P-PSDB; ABG00399

30-MAR-2001; 2001WO-US008631

WO200175067-A2

11-OCT-2001

Homo sapiens

2000US-00540217 2000US-00649167

31-MAR-2000; 23-AUG-2000;

gene therapy;

(first entry)

/*tag= a /product= "Clone THYMU20071120 protein"

Location/Qualifiers 170. .1792

61 CGTCCCAAAAAGTATATTTGCACATATGAAGGGTGTGATAAAAGCCTATAATCGACCATCA 120

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tissue regeneration, cell regeneration, membrane protein;
signal transduction-related protein; transcription-related protein;
osteoporosis; neurological disease; cancer; tumour.
                                 Human; 88; gene; pharmaceutical; diagnostic;
                       Human cDNA encoding clone THYMU20071120,
                                                                                                                                                       (HELI-) HELIX RES INST.
(REAS-) RES ASSOC BIOTECHNOLOGY.
                                                                                                                                      05-NOV-2001; 2001JP-00379298.
25-JAN-2002; 2002US-00353978.
                                                                                                                           28-MAR-2002; 2002EP-00007401
                                                              sapiens
                                                                                                     EP1308459-A2
           04-DEC-2003
                                                                                                                07-MAY-2003
                                                                                                                                                                              Yamamoto J,
ADB63624;
                                                                                                                                                                                    Seki N,
                                                                                                                                                                         Isogai
                                                             Ношо
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The invention discloses a polymucleotide comprising a sequence selected from 1970 fully defined nucleotide sequences which encode novel polypeptides. Also claimed its a polypeptide encoded by the polymucleotide or its partial peptide, an antibody binding to the polypeptide or peptide of the polymucleotide by consecting the polypeptide or peptide with the antibody of the encoded protein, and observing the binding between the two a transformant carrying the polymucleotide in an expressible manner and an antisense polymucleotide, or as a probe of the section as a primer for synthesiang the polymucleotide, or as a probe for detecting the polymucleotide. The oligonucleotide is useful as a primer for synthesiang the polymucleotide and encoded for detecting the polymucleotide. The polymucleotide and encoded is useful as pharmaceutical agents and marker or medicines for regulation of their expression and activity, or as targets of genes may be included in them, for developing a diagnostic marker or medicines for regulation of their expression and activity, or as targets of gene therapy. The genes are involved in tissue and/or cell respection. Membrane proteins, disease-related proteins, transcription-related proteins, disease-related proteins, transcription-related proteins, disease-related proteins and genes encoding them can be used as indicators for diseases (e.g. osteoporosis, neurological diseases, cancer, tunours. The cDNA may be used to regulate the activity or expression of the encoded protein to treat diseases. The sequence presented is a cDNA of the invention Note: Some of the sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the European Patent Office.
Otsuki T, Wakamatsu A, Sato H, Ishii S;
Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
Otsuka M, Nagahari K, Masuho Y;
                                                                                                                                                                                                                                                                                                                                                                                                              New polynucleotides and polypeptides, useful for devaloping a diagnostic marker or medicines for regulation of their expression and activity, or as targets of gene therapy.
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7.4%; Score 91.8; DB 9; Length 2110;
Best Local Similarity 51.7%; Pred, No. 1e-08;
Matches 314; Conservative 0; Mismatches 277; Indels 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page; 222pp; English.
., Sugiyama T,
J, Isono Y, H
Yoshikawa T, O
                                                                                                                                                                                                                                          2003-450961/43.
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Gaps

16;

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1253 CATACCGAAGAGAAACCCTACAAATGTAAAGAATGTGGGAAAGCTTTTAAACACTCCTCA 1312
                                                                                                                                                                    1367 GAATGTGGCAAAGCTTTTAACCGATCCTCAAAACTTACTGAACATAAGAAACTTCATACT 1426
                                                                                                                                                                                                                                                1427 dgakagakaccinacakancingakcanteresekakacintrikinggakanccinaakacin 1486
                                                                                                                                                                                                                                                                                                                               1487 ACTGAACATAAAAAAATTCATTCTGGAGAGATACCCTACAAGTGTGAAGAATGTGGGAAA 1546
                                                                                                                                                                                                                                                                                                                                                                                                              1547 GCTTTTAAACACTCCTCATCCCTTACTACACATAAAAGAATTCATACTGGGGAAAAACCC 1606
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                                                                                     .313 GCCCTTACTACACATAAGAGAATTCACACTGGAGAGAAACCCTACAAATGT-----GAA 1366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1607 TACAAATGTGAAGAATGTGGCAAAGCTTTTAGCCGATCCTCAAAACTTACTGAACATAAG 1666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1667 ATAATTCATACTGGAGAGAAACCCTATAAATGTGAGAGATGTGACAAAGCTTTTAACCAA 1726
                                                                                                                                                                                                                                                                                          301 AAAAGACATGAAATCACCCATACAAAGTCATTTAAATGTACATTTGAAAATTGTCAAGAA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 597 ICCTABATGTGGTABAGGTTGTGTTTGGGBABABAGGTTTATCTTCACATATGTTBAGTCA 656
                                                121 TTATTAGAGCAACATTTAAGAACCCACAGTAATGATCGACCGTATAAATGTACAGTGGAC 180
                                                                                                                            181 GATTGTGATAAAGCATTTTTCAGAAAATCACATTTGGAAACACATATTGTATTACAATTCC 240
                                                                                                                                                                                                           241 GAAAAAACCATTCCATTGTTCAGTGTGTAAAGGGGTTAATTCTCGACAACACTTG 300
                                                                                                                                                                                                                                                                                                                                                                      361 GCATTTTATAAACATCAATCTTTA---AGACATCATATATTATCTGTTCATGAAAAAAAA 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                     418 TTAACGIGTAAACAATGTAATAAAGTTTTCACTCGACCTTCAAAATTAGCACAACATAAA 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITCCAAACTIGGICAGIAITACAATITCATAIAAAACAACIGCAICCAAAACTIAAAIG 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human; macroprotein-45.76; dementia; arrhythmia; asthma; diabetes; ss;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      478 TTAAAACATCATGGTG-GATCTCCTGCTTATCAATGTGATCATCCTGGTTGTTTTAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= a
/product= "Human macroprotein-45.76"
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180. .1430
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The invention discloses a polynucleotide comprising a sequence selected from 1970 fully defined nucleotide sequences which encode novel or its partial peptide, an antibody binding to the polypeptide or peptide or the polynucleotide, immunologically assaying the polypeptide or peptide or peptide by contacting the polypeptide or peptide or peptide by contacting the polypeptide or peptide or the polynucleotide by contacting the polypeptide or peptide or with the antibody of the encoded protein, and observing the binding or expressible manner and an antisense polynucleotide. The oligonucleotide is useful as a primer for synthesising the polynucleotide, or as a probe of or detecting the polynucleotide. The polynucleotide, or as a probe or suseful as pharmaceutical agents and encoded or proteins are useful as pharmaceutical agents and mand agence or genes may be included in them, for developing a diagnostic marker or medicines for regulation of their expression and activity, or as targets or genes are involved in tissue and/or cell or regeneration. Membrane proteins, disease-related proteins and expression of the encoded proteins and as a probe or concoding them can be used as indicators for diseases (e.g. osteoporosis, the activity or expression of the encoded protein to treat diseases. The concoding them can be used as indicators for diseases (e.g. osteoporosis, the activity or expression of the encoded protein to treat diseases. The sequence presented is not represented in the printed specification, but is based on sequence information supplied by the Buropean Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ishii S;
, Tamechika I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polynucleotides and polypeptides, useful for developing a diagnostic marker or medicines for regulation of their expression and activity, or as targets of gene therapy.
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tissue regeneration; cell regeneration; membrane protein;
signal transduction-related protein; transcription-related protein;
osteoporosis; neurological disease; cancer; tumour.
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iio Y, Otsuka K, Nagai K, Irie
Otsuka M, Nagahari K, Masuho Y;
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                                                                                                                                                                                                                                    /product= "Clone FEBRA20063720 protein'
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                                                                                                                                                             Location/Qualifiers
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(REAS-) RES ASSOC BIOTECHNOLOGY.
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25-JAN-2002; 2002US-00350978.
                                                                                                                                                                                   118. .1878
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Yamamoto J, Isono Y,
Seki N, Yoshikawa T,
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCTACAAATGTGAAGAATGTGGCAAAGCTTTTAACCGGTCCTCAACCTTACTAAACATA 1005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAAGAATTCATACAGAAGAAACCCTACAAATGTGAAGAATGTGGCAAGGCCTTTAACC 1065
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                                                                                                                                                                                                                                                                                                                                                The invention relates to a novel human macroprotein-45.76, the encoding polymiclectide, an antagonist and a method of recombinant production. The protein of the invention may be useful for treating dementia, arrhythmia, asthma and diabetes. The current sequence is that of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Groscadarcarrrrecardecrrrrecadarradacreadaradadadararrecardade 771
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGTATICITACAAATGIGAAGAATGIGGTAAAGCCITTAACTGGTCCTCAACCCTTACTA 831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AACAITITAAGAACCCACAGTAATGATCGACGGTATAAATGTACAGTGGACGATTGTGATA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AACATAAGATAATTCATACTGGAGAAAAGCCTACAAATGT-----GAAGAATGTGGCA 885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATTCCATTGTTCAGTGTGGTAAAGGGGTTAATTCTCGACACACTTGAAAAGACATG 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              311 AAATCACCCATACAAAGTCATTTAAATGTACATTTGAAAATTGTCAAGAAGCATTTAATA 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70
                                                                                                                                                                                   New human macroprotein-45.76, encoding polynucleotide, antagonist and recombinant production, useful for treating dementia, arrhythmia, asthma and diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GIGACGAAACCAAAICGAIAICAICITIAAIAITCIICTICTICTICAICACGICCCAAAA
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ص
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 2760;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2760 BP; 1016 A; 463 C; 499 G; 782 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches 227; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.4%; Score 91.8; DB 9; 32.1%; Pred, No. 1.1e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              macroprotein-45.76 cDNA of the invention.
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                   DEV INC SHANGHAI
                                                                                                                                                                                                                                                                                                       Chinese
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52.1%;
                                                                                                                                                                                                                                                                                                       NO 1; 34pp;
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ses 257; Conservative
                        BIOWINDOW GENE
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                                                                                                                            WPI; 2003-269486/27.
                                                                                                                                                  P-PSDB; ADC56696
                                                                                                                                                                                                                                                                                                         Claim 6; SEQ ID
                                                                       Xie Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         371
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                        (BIOM-)
                                                                       Mao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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1004 AGTTCTCGATTCTTAATAAACATAAGAGAATTCATATGGAAGATAAACCCTACAAATGTG 1063
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AACATTTAAGAACCCACAGTAATGATCGACGGTATAAATGTACAGTGGACGATTGTGATA 190
                                                                                                                                 CATTCCATTGTTCAGTGTGTGTAAAGGGGTTAATTCTCGACAACACTTGAAAAGACATG 310
                                                                                                                                                                  cenacaaardreaagaardreecaaagerrriraacegereercaaceerraacara 943
                                                                                                                                                                                                   311 AAATCACCCATACAAAGTCATTTAAATGTACATTTGAAAATTGTCAAGAAGCATTTTATA 370
                                                                                                                                                                                                                                                                     AACAICAAICITI---AAGACAICAIAIAITIAICIGIICAIGAAAAACAIIAACGIGIA 427
                                                                                                                                                                                                                                                                                                                                     428 AACAATGTAATAAAGTTTTCACTCGACCTTCAAAATTAGCACAACATAAATTAAAACATC 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; nucleic acid associated protein; NAAP; stroke, AIDS; nootropic, cancer; atherosclerosis; neurological; epilepsy; Huntington's a disease; developmental disorder; antiinflammatory; neuroprotective; thyromimetic; Cushing's syndrome; infection; gene therapy; cytostatic; anticonvulaent; cerebroprotective; hypothyroidism; cell proliferative disorder; allergy;
                               770 AACATAAGATAATTCATACTGGAGAAAAACCCTACAAATGT-----GAAGAATGTGGGA
                                                                 AAGCATTTTTCAGAAATCACATTTGGAAACACATATTGTATCACATTCCGAAAAAAA
                                                                                                Griffin JA, Tang YT;
Lu DAM, Forsythe IJ;
Sanjanwala MM, Lee EA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human nucleic acid associated protein (NAAP) -34 cDNA.
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/product= "Human NAAP protein"
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Yue H, Baughn MR, Emerling BM, Lal PG,
Ramkumar J, Li JX, Becha SD, Duggan BM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAD55863 standard; cDNA; 2026 BP.
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13-JUL-2001; 2001US-0305335P.
13-JUL-2001; 2001US-0305390P.
19-JUL-2001; 2001US-0306960P.
20-JUL-2001; 2001US-0306694P.
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1002 gaargriggcaaagccrrcraccarrcrrcacaccrracracacaraaggraarrcaracr 1061
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   246
                                                                                                                                                         New human nucleic acid associated proteins (NAAP), useful for diagnosing, treating and preventing diseases or conditions associated with the aberrant NAAP expression e.g. cancer, AIDS, atherosclerosis, epilepsy, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 AAAAAGTATATTTGCACATATGAAGGGTGTGATAAAGCCTATAATCGACCATCATTATTA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGTAAACAATGTAATAAAGTTTTCACTCGACCTTCAAAATTAGCACAACATAAATTAAAA 483
                                                                                                                                                                                                                                                                                                                 The invention relates to human nucleic acid associated proteins (NAAP) and their corresponding nucleic acid sequences. The invention is useful in diagnosing, treating and preventing diseases or conditions associated with the decreased expression or overexpression of NAAP, such as sociated proliferative (e.g. cancer, atherosclerosis), neurological (e.g. proliferative (e.g. disease, stroke), immune/inflammatory (e.g. AIDS, allergies) and developmental (e.g. Hypothyroidism, Cubiling's syndrome) disorders, or infections. It is also useful in assessing the effects of exceptions compounds on the expression of nucleic acid and amino acid sequences of NAAP. The NAAP or its fragments are useful in screening compounds for which acts as their agonist or antagonist. The microarray is useful in monitoring or measuring protein-protein interactions, and gene expression profiles. NAAP DNA is used in gene therapy. The present sequence is human NAAP CNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 GAAAGIGACGAAACCAAAICGAIAICAICTTIAAIAICIICTICTICAICAICACGICCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      127 GAGCAACATTTAAGAACCCACAGTAATGATCGACCGTATAAATGTACAGTGGACGATTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   187 GATAAAGCATITITCAGAAAATCACATITGGAAACACATAITGTATCACATTCCGAAAAA
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Yao MG;
Lu Y;
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  Borowsky ML,
Nguyen DB,
Elliott VS, Ison CH, Ding L, B
Tran B, Walia NK, Hafalia AJA,
                                                                                                                                                                                                                                                                           Claim 5; Page 259-260; 260pp; English.
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                                                                                          WPI; 2003-221732/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                 P-PSDB; AAE37047
Burford N,
Barroso I,
                                                                                                                                                                                                                                   infections.
                                               Arvizu CS;
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RESULT 13

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1438 TGTGAAGAATGTGGCAAAGCCTTTAACCACTCCTCAAAACTTACTATACATAAGATAATT 1497
                                                                                                                                  1378 AATGTGTCTTCACACCTTACTACACATAAGATGATTCATACTGGAGAAAACCCTACAAA 1437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Otsuki T, Wakamatsu A, Sato H, Ishii S;
Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
Otsuka M, Nagahari K, Masuho Y;
                                                                                   367 TATAAACAT---CAATCTTTAAGACATCATATATTATCTGTTCATGAAAAACATTAACG 423
                                                                                                                                                                                    424 TGTAAACAATGTAATAAAGTTTTCACTCGACCTTCAAAATTAGCACAACATAAATTAAAA 483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cytostatic, Anti-inflammatory, Osteopathic, Neuroprotective, Nootropic, Gene Therapy, human, secretory protein, membrane proteins, cancer; inflammatory disease, osteoporosis, neurological disease, gene, ss.
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                                                                                                                                                                                                                                                                                                                                          1498 CATACTGGAGAGAAACCT 1515
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(REAS-) RES ASSOC BIOTECHNOLOGY.
                                                                                                                                                                                                                                                                                        484 CATCATGGTGGATCTCCT 501
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24-JAN-2002; 2002US-0350435P.
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Seki N, Yoshikawa T,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polynucleotides encoding full-length polypeptides, e.g. secretory and/or membrane proteins, useful for developing medicines for diseases in which the gene is involved, or as target molecules for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 187 GATAAAGCATTTTTCAGAAAATCACATTTGGAAACACATATTGTATCACATTCCGAAAAA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67 AAAAAGTATATTTGCACATATGAAGGGTGTGATAAAGCCTATAATCGACCATCATTATTA 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 GAAAGTGACGAAACCAAATCGATATCATCTTTAATATCTTCTTCTTCTTCATCACGTCCC 66
                                                                                                                                                                                                                              Cytostatic, Anti-inflammatory, Osteopathic, Neuroprotective, Nootropic, Gene Therapy, human, secretory protein, membrane proteins, cancer, inflammatory disease; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to novel human secretory or membrane process (ADA5407). ADA55710) and their coding sequences (ADA5433-ADA54071). The coding sequences are useful in the gene therapy of diseases caused by abnormalities of the proteins, e.g. cancer, inflammatory diseases, osteoporosis or neurological disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 692; 205pp; English.
                                                                                                                                                                                    Human coding sequence, SEQ ID 692.
                        ADA53124 standard; cDNA; 2114 BP.
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(REAS-) RES ASSOC BIOTECHNOLOGY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-SEP-2001; 2001JP-00328381.
24-JAN-2002; 2002US-0350435P.
                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; ADA54763.
                                                                                                                                                                                                                                                                                                                                                                                         EP1293569-A2.
                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                               20-NOV-2003
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                                                                                ADA53124;
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67 AAAAAGTATATTTGCACATATGAAGGGTGTGATAAAGCCTATAATCGACCATCATTATTA 126
                                                                             716 AGAGAGAATTTCTACAAATGTGAAGAGTGTGGAAAAACCTTTAACTGGTCCACAAACCTT 775
                                                                                                                                                                                                                                                                                                                                        GATAAAGCATTTTTCAGAAAATCACATTTGGAAACACATATTGTATCACATTCCGAAAAA 246
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                                                                                                                                                               GAGCAACATTTAAGAACCCACAGTAATGATCGACCGTATAAATGTACAGTGGACGATTGT
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Human; diagnostic; drug screening; forensics; gene mapping; blodiversity assessment; Parkinson's disease; Alzheimer's disease; neurodegenerative diseases; anaemia; platelet disorder; wound; burns; ulcers; osceoporosis; autoimmune disease; cancer; molecular weight marker; food supplement; antiparkinsonian; nootropic; neuroprotective; antianaemic; anticoagulant; thrombolytic; vulnerary; antiulcer; osceopathic; immunosuppressive; antiinflammatory; cytostatic; gene therapy; chromosome 19q12; gene; ss. Wang J, Zhao QA, Human novel cDNA sequence, SEQ ID NO:844. Ren F, Xue AJ, ADC30762 standard; cDNA; 2064 24-SEP-2002; 2002WO-US030474 24-SEP-2001; 2001US-0324631P 18-DEC-2003 (first entry) Zhang J, (HYSE-) HYSEQ INC. WO2003029271-A2. Ното варіеля 10-APR-2003 ADC30762; Tang TY, RESULT 15

The invention relates to 971 novel human cDNA sequences (ADC29919-ADC 18099) and the polypeptides they encode (ADC30800-ADC31860). The ADC30800 human cDNAs. The invention additionally encompasses expression the novel human cDNAs. The invention additionally encompasses expression the novel human cDNAs. The invention additionally encompasses expression to be novel human cDNAs. The invention and encloded of the invention; an antibody against a polypeptide of the invention; and methods of polymertical conditions and methods of detecting polymertical conditions and methods of invention and methods of invention and methods of invention and methods of invention and methods of carrying a compound which bins to a polypeptide of the invention. The invention further discloses methods of peventing, treating or ameliorating a medical condition; kits comprising polymercial probes of invention methods for the onlymercial of compounds that modulate the appreciation or activity of the polymercial of compounds that modulate the expression or activity of the polymercial of compounds that modulate the expression or activity of the polymercial of compounds that modulate the expression or activity of the polymercial of compounds that modulate the expression or activity of the polymercial of compounds that modulate the expression or activity of the polymercial of compounds that modulate the expression of disporters or other traits, for assessing biodiversity, and in producing many other types of disease and other neurodegenerative diseases, anomia, platelet concern the nucleic acids may also be used to protein. The polymeric of also used for treatling diseases such as Parkinson's diseases or cancer. The nucleic acids may also be used of a protein. The polymeric of the invention of a protein. The sequence date for this patent did not form part of the printed specification, but was an electronic form that the requence of the invention of a protein or but wis patent did not form mat the requence of the printed specification, but we have treating conditions such as neurodegenerative diseases, anemias, platelet disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or New polynucleotide and polypeptide useful for diagnosing, preventing or Weng G; Wang Z, Asundi V, Claim 1; SEQ ID NO 844; 1185pp; English. Ma Y, Drmanac RT; Wang D, WPI; 2003-371981/35. Ghosh M, Haley-Vicente D, P-PSDB; ADC31733

Gaps 9. Length 2064; Sequence 2064 BP; 703 A; 375 C; 449 G; 537 T; 0 U; 0 Other; 53.7%; Pred. No. 3.4e-08; live 0; Mismatches 193; Indels 7.2%; Score 89.2; DB 9; Local Similarity 53.7 es 234; Conservative Query Match

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366 TIATAAACATCAATCTTTAAGACATCATATTATTATCTGTTCATGAAAAAACATTAACGTG 425

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Search completed: May 9, 2004, 06:07:07 Job time : 549.661 secs

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1 atgagtgaaagtgacgaaac.....catcagtgatttctcgataa 1239
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(c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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BC036394 Homo sapi AQ006136 CTT-HSP-2 B99387 CTT-HSP-2 BC022527 Homo sapi BC028252 Homo sapi BC028252 Mus muscu BE161630 MR3-H7044 BC022590 Homo sapi AX03301 Mus muscu BX456765 BX456765 BX456765 BX456765 BX437291 BX437291 BX35654 BX437291 BX35654 BX437291 BX35654 BX437758 AQ347265 RPCIII-I1 AQ38266 RPCIII-I1 AQ3826 RPCIII-I1 BX35654 BX437758 AQ347265 CTTE-E1-AQ19427 AGENCOURT AQ19427 AGENCOURT AQ19427 AGENCOURT AQ19427 HOMO SAPI AQ19428 RPCIII-61 AQ19437 AGENCOURT AQ19427 HOMO SAPI AQ19428 RPCIII-61 AQ19427 HOMO SAPI CAB74049 MOSQ28DI-BG65056 GO2668829 BUJ1453 AGENCOURT CAB74049 MOSQ28DI-BC020045 HOMO SAPI CAB7404 AGENCOURT CAB7404 MOSQ28DI-BC13434 AM30402 AGENCOURT CAB7404 MOSQ28DI-BC135920 UI-HF-BNO AG184274 AGENCOURT CAB7449 MR2-CI012 CAB7444 MOSQ28DI-BF817669 MR2-CI012 CAB7444 AGENCOURT CAB7444 AGENCOURT CAB7444 AGENCOURT CAB7444 AGENCOURT CAB7444 AGENCOURT CAB7444 AGENCOURT CAB7444 AGENCOURT CAB7444 AGENCOURT CAB7444 AGENCOURT CAB7444 AGENCOURT CAB7444 AGENCOURT CAB7444 AGENCOURT CAB7444 AGENCOURT CAB7444 AGENCOURT CAB7444 AGENCOURT CAB7444 AGENCOURT

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BC022527 BC037782 BC037782 BC032590 AL705393 AK033001 AK033958 BC195416 BX45765 BC195416 BX45765 BC195416 BX45765 BC195416 BX35765 BC195416 BX35765 BC195416 BX35765 BC195416

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628 bp DNA linear GSS 31-OCT-2002 (GSS) 1-OCT-2002                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGS.
Candida glabrata
Candida glabrata
Candida glabrata
Eukaryota; Fungl; Ascomycota; Saccharomycetes;
Saccharomycetales; Candida.
1 (bases I to 628)
Wong, S., Fares, M.A., Zimmermann, W., Butler, G. and Wolfe, K.H.
Evidence from comparative genomics for a complete sexual cycle in the Assexual pathogenic yeast Candida glabrata
Genome Biol. 4 (2), R10 (2003)
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Contact: Wong S
Contact: Wong S
Department of Genetics, Smurfit Institute
Trinity College Dublin
Dublin 2, Ireland
Tel: 353 1 6082319
Fax: 353 1 6798558
Email: swong@tcd.ie
Class: plasmid ends.
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BZ298000 CG3957.fl AL405671 T7 end of AK032220 Mus muscu BC047646 Homo sapi

BZ298000 CNS06MMP AK032220 BC047646

11338

628 959 1609 2647

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182.2 167.6 98.2 97.8

No.

ALIGNMENTS

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Saccharomyces kluyveri
FBBS Lett. 487 (1), 56-60 (2000)
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(bases 1 to 959)
Souciet, J. L., Aigle, M., Artiguenave, F., Blandin, G.,
Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,
Andermonismy, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B.,
Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
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                                                                                       /db_xref="taxon:5478"
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/clone_lib="Candida glabrata Random Genomic Library'
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0; Mismatches 228; Indels
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                                    /organism="Candida glabrata"
/mol_type="genomic DNA"
/strain="CBS 138"
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Direct Submission

Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,

2 rue gaston Cremieux, CP 5706, 91057 EVRX cedex, FRANCE. (B-mail:

2 rue gaston Cremieux, CP 5706, 91057 EVRX cedex, FRANCE. (B-mail:

2 rue gaston Cremieux, CP 5706, 91057 EVRX cedex, FRANCE. (B-mail:

8 seqref@genoscope.cns.fr - Wab: www.genoscope.cns.fr)

This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces barnus var. uvarum, Saccharomyces

exiguus, Saccharomyces servazii, Zygosacharomyces rouxii,

Saccharomyces Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Rluyveromyces maxxianus var. marxianus, Pichia angusta. Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarromya lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

Location/Qualifiers

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Wincker, P. and Weissenbach, J.
Genomic exploration of the hemiascomycetous yeasts:
yeast species for molecular evolution studies
FEBS Lett. 487 (1), 3-12 (2000)
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1; Mismatches 235; Indels
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/mol_type="genomic DNA"
/strain="CBS 3082"
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polyA_signal
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Mus musculus adult male olfactory brain cDNA, RIKEN full-length enriched library, clone:6430503015 product:MSZF33 (FRAGMENT) homolog [Mus musculus], full insert sequence.

AK032220

AK032220.1 GI:26328050

HIC; CAP trapper.

Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Yanni,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsunoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Yoneda,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKBN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The FANTOM Consortium and the RIKEN Genome Exploration Research Choup Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length CDNAs
Nature 420, 563-273 (2002)
6 (Dases 1 to 1609)
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Haraoka,T., Haraoka,T., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hiraoka,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
624
                                         598 CATATCAAGGCGGACCATCCCAAGTTGCACTGTAACGTATGTGGCCAAAGCTTGTGTTGTTGT
                                                                                        684
                                                                                                                                                                              685 ACTIGIGATIATIGIGATGTGGGGAAATTTGCAAAGAAAAATGAATTAGTTGAACATTAT 744
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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CATATAAAACAACTGCATCCAAAACTTAAATGTCCTAAATGTGGTAAAGGTTGTGTTGGG
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Nature 409, 685-690 (2001)
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, N., Murata, M., Nakama, M., Nakama, T., Miyazaki, R., Murata, M., Nakami, M., Nahi, K., Nomura, K., Numazaki, R., Chno, M., Ohsato, N., Okazaki, Y., Saito, R., Saito, H., Sakai, K., Saitaki, T., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shizaki, T., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takaka, Y., Tanaka, M., Tomaru, A., Toya, T., Takaku-Akahira, S., Direct Submission Hyashizaki, Y. Toya, T., Yasunishi, A., Direct Submission Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Submitted and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (B-mail:genome-res@gec.riken.go.]p, Fax:81-45-503-9216)
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/broteIn_id="BAC27766.1"
/backeIn_id="Los3280x1"
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NKAFYJESYLQVHKKTHTGEKPYKCNECGKAPARSHLKVHKITHTGEKPYKCNQCGK
ALAAYHSTLQVHQRTHTGEKPYECBQCGKAFANQSYFQVHKRIHTGEKPYKCDQCGKAP
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clone lib="RIKEN full-length enriched mouse cDNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rike Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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[Mus musculus] (SPTR|088251, evidence: FASTY, 87.1%ID,
100%length, match=255)
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Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
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51.2%; Pred. No. 1.5e-08;
ive 0; Mismatches 283;
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(db_xref="MG1:2355676"

db_xref="taxon:10090"

(clone="6430503015"
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/mol_type="mRNA"
/strain="C57BL/6J"
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'note="putative"
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With-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1409 GGCAAAGCCTTTAAGCAGTCCTCAAACCTTACTACATAAGATAATTCATACTGGAGAG 1468
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Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Klausner, R.D., Collins, F.S., Wagner, L., Shemmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Staplecon, M., Soares, W.M. B., Bonaldo, M.F., Casavant, T.L.,
Scheez, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Boast, S.A., McZwan, P.J.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodersen, E.D.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Kzzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.B., Jones, S. J. and Marra, M.A.
Generation and mouse oDNA sequences
L. Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BC047646 Howo sapiens zinc finger protein 85 (HPF4, HTF1), mRNA (cDNA clone MADE:4828290), with apparent retained intron.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            992 ATATCATAGTACACTCCAAGTACATGAAAGAACACATACTGGAGAGAAGCCCTATGAATG 1051
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               240 CGAAAAAACCATTCCATTGTTCAGTGTGTGTGTAAAGGGGTTAATTCTCGACAACACTT 299
                                                                                                                                                                                                                                                                                          rcahahachrehahanahchchrachgagaganahacrrrachagagargharahah 814
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 2647)
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Direct Submission
Submitted (03-MAR-2003) National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                           AGCATTT - - TATAAACATCAATCTTTAAGACATCATATATTATCTGTTCATGAAAAAC
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                                                                                                          GABABGACATGABATCACCCATACABGTCATTTABATGTACATTTGABABATTGTCAAGA
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Homo sapiens (nument)

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

I (bases lto 2672)

Straubberg, R.D., Colling, F.S., Wagner, L.D.H., Derge, J.G.,

Altschul, S.D., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Altschul, S.P., Jordan, H., Moore, T., Max, S.L., Wang, J., Haleh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.B., Brownsteah, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Rah, S.S., Loquellano, N.A., Peters, G.J.,

Morley, K.C., Hale, S., Guratane, P.H., Richards, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, Y., Gibbs, R.A.,

Sanchez, A., Whiting, M., Madan, A., Youug, A.C., Shevchenko, Y.

Butfard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

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Butterfield, Y.S., Krzywinski, M.I., Salska, U., Smailus, D.E.,

Butterfield, Y.S., Krzywinski, M.I., Salska, U., Smailus, D.E.,

Butterfield, Y.S., Krzywinski, M.I., Selska, U., Smailus, D.E.,

Butterfield, Y.S., Krzywinski, M.I., Selska, W., Smailus, D.E.,

Butterfield, Y.S., Krzywinski, W., Sung, S.S.,

Butterfield, Y.S., Spain, J
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Homo sapiens zinc finger protein 85 (HPF4, HTF1), mRNA (cDNA clone
IMAGE:5259399), containing frame-shift errors.
                                                                                                                                                                                               381 carcacarantrcaracregagagagagaacccracaargregaaaargregaaaagccrrr 440
                                                                                                                                                                                                                                                              367 TATAA---ACATCAATCTTTAAGACATCATATATTATCTGTTCATGAAAAACATTAACG 423
                                                                                                                                                                                                                                                                                                                             441 AATCATTTCTCACACTTACTACACATAAGATAATTCATACTGGAGAAACCTTACAAA 500
   247 AAACCATTCCATTGTTCAGTGTGTGAAAGGGGTTAATTCTCGACAACACTTGAAAGA 306
                                                                  321 AAACCCTACAAATGTAAAAAATGTGGAAAAGCCTTTAACCAGTCTGCACACCTTACTACA 380
                                                                                                                                                                                                                                                                                                                                                                                            424 IGTAAACAATGTAATAAAGTTTTCACTCGACCTTCAAAATTAGCACAACATAAATTAAAA 483
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Submitted (05-AUG-2002) National Institutes of Health, Mammalian
Gene Collection (MCC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              544 ACTIGGTCAGTATTACAATTTCATATAAAACAACTGCATCCAAAACTTAAATGTCCTAAA
                                                                                                                                    CATGAAATCACCCATACAAAGTCATTTAAATGTACATTTGAAAATTGTCAAGAAGCATTT
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NIH-MGC Project URL: http://mgc.nci.nih.gov
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                                                           1769 AAACTTACTGAACATAAGAAATTCATACTGGAGAGAAACCCTA---TGAATGTGAAAAA 1825
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/note="Vector: pME188FL3; mRNA from uninduced NT2 neuronal
precursor cells"
ACTIGGICAGIAITACAATITICATATAAAACAACIGCATCCAAAACTIAAAIGICCIAAA 603
                                                                                                                                                                                  1826 IGIGGCAAAGCTTTTAACCAGTCCTCAAATCTTACTAGACATAAGAAAAGTCATACAGA 1884
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Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 745)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project, 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ota, T., Wakamatsu, A., Ozawa, M., Ishii, S., Saito, K., Yamamoto, J., Nakamura, Y., Nishikawa, T., Nagai, T., Suzuki, Y., Sugano, S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 AAAAAGTATATTTGCACATATGAAGGGTGTGATAAAGCCTATAATCGACCATCATTATTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NT2RM2000319"
/cell_type="texatocarcinoma"
/cell_line="WT2"
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Unpublished (1998)
Other GSSs: GTT-HSP-2290017.TR
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Contact: Mark Adams
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Contact: Mark Adams
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The Institute for Genomic Research
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Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seg primer: M13-21;
Class: BAC ends.
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                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I Chases I to Sal. Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K. Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Vencer, J.C.
Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="Male"
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HindIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 591;
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Pred. No. 2.4e-07;
0; Mismatches 225; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic_DNA
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al Similarity 52.2%;
256; Conservative (
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Location/Qualifiers
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                  Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shira
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: anadandsystemsbiology.org
Anup Madan, Jessica Pahey, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
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Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BP 191 9106 EVRY cedex - France
BP 191 9106 EVRY cedex - France
Email: seqref@genoscope.cns.fr,
Invitrogen. This sequence belongs to sequence cluster 9703.f For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?eeq=CSOCAP001DB06QP1&cluster=9703.f. Contact:
Feng Lang Email: fliangeliferech.com URL:
http://lullength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSOCAP001DB06QP1.
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                                                                                                                             341 CCAGTCCTCAACTCTTAGAAACATGAGATAATTCATACTGGAGAGAAACCTTACAAATG 400
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1. (bases 1 to 1163)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full.length cDNA libraries and normalization

Unpublished (2001)
                                                                                                                                                                                                  426 TAAACAATGTAATAAAGTTTTCACTCGACCTTCAAAATTAGCACAACATAAATTAAAACA
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BX414627 Homo sapiens THYMUS
5-PRIME, mRNA sequence.
BX414627, GI:30649903
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Contact: Mark Adams
Contact: Mark Adams
Contact: Mark Adams
Contact: Mark Adams
Contact: Mark Adams
Contact: Mark Adams
Contact: Mark Adams
The Institut of Eukaryctic Genomics Research
712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0208
Email: madamm@@tigr.corg
Clones are available from Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.corg/tdb/humgen/bac_end_search/bac_end_search.html
Seg primer: M13-21;
Class: BAC ends.
                                                                                                                                                                                                                                                                      B99387 Linear GSS 26-JUN-1998 CIT-HSP-2281A10.TF CIT-HSP Gapiens genomic clone 2281A10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutleleostomi; Mammalia; Eutleria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2)

Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.

Use of a random BAC End Sequence Database for Sequence-Ready Map

Building (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ?
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            107 AAAACATGAGATAATTCATACTGGAGAGAAACCCTACAAATGT-----GAAGAATGTGG 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         189 TAAAGCATTTTTCAGAAATCACATTTGGAAACACATATTGTATCACATTCCGAAAAAAA 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             220
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/clone_lib="CIT-HSP"
//note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
HindIII"
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/mol_type="genomic DNA"
/db_xref="GDB:7147044"
/db_xref="taxon:9606"
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les 231; Conservative
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                                       484 CATCATGGTG 493
                                                                                                    543 CATACTGGAG 552
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BC022527

2694 bp mRNA linear HTC 19-NOV-2003

Homo sapiens hypothetical protein LOC148206, mRNA (cDNA clone
LIMAGE:4797857), containing frame-shift errors.
GTGGTAAAGGGGTTAATTCTCGACAACACTTGAAAAGACATGAAATCACCCATACAAAGT 328
                         295 GIGGAAAAGCCTITAACCAGICTGCACACCTIACCACACACACATGAGGIAATTCATACTGGAG 354
                                                                   CATTIAAAIGIACAITIGAAAAIIGICAAGAAGCAITITIAIAA---ACAICAAICITIAA 385
                                                                                                                                                                             474
                                                                                                                                                                                                            TCACTCGACCTTCAAAATTAGCACAACATAAAATTAAAACATCATGGTGGATCTCCTGCTT 505
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                                                                                                                                                                                                                                                                                                                                                      566 ATATAAAACAACTGCATCCAAAACTTAAATGTCCTAAATGTGGTAAAGGTTGTGTTGTGTTGGGA 625
                                                                                                      355 AGAAACCCTACAAATGTGAAAGATGTGGAAAAGCCTTTAATCATTTCTCACACCTTACTA 414
                                                                                                                                                                                                                                                                                                                    535 AATGTAAAGRATGTGAAAGAGCTTTTAACCAATCCTCAAAACTTACTGAACATAAGARAA 594
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Submitted (01-FEB-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2550,
USA
                                                                                                                                      386 GACATCATATATTATCTGTTCATGAAAAACATTAACGTGTAAACAATGTAATAAAGTTT
                                                                                                                                                                       415 CACATAAGATAATTCATACTGGAGAGAAACCTTACAAATGTAAAGRATGTGGTAAAGCTT
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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BC022527.1 GI:18490307
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NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Bmail: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki
Toshiyuki and Plero Carninci (RIKEN)
DNA Library Arrayed by: The I.M.AG. Consortium (LIML)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Contact; Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiML at: http://image.llnl.gov Series: IRAK Plate: 32 Row: f Column: 2 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein
This clone has the following problem: frame shifted.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    424 IGIAAACAATGIAATAAAGTTTTCACTCGACCTTCAAAATTAGCACAAAAATTAAAA 483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 7.3%; Score 90.4; DB 11; Length Local Similarity 51.8%; Pred. No. 4.1e-07; Indepense 258; Conservative 0; Mismatches 231; Indels use 258; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
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/rissue=type="Brain, hypothalamus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
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Leases I. C. 2698'

Strausberg, R.L., Ferngold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Magner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buercow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.B., Brownstein, M.J., Usduellano, N.A., Peters, G.J.,
Abrameon, R.D., Mullahy, S.J., Bosak, S.A., McKwan, P.J.,
McKernan, K.J., Malk, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Sak, M.K., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Young, A.C., Shevcherko, Y.,
Baucher, A., Whiting, M., Madan, A., Young, A.C., Shevcherko, Y.,
Bouckernd, G., Blakesley, R.W., Touchman, J.W., Schentz, J., Myers, R.M.,
Schnerth, A., Schein, J.E., Jones, S.J. and Marra, M.A.,
Schnerth, A., Schein, J.E., Jones, S.J. and Marra, M.A.,
Schnerth, A., Schein, J.E., Jones, S.J. and Marra, M.A.,
Brock, Mall, Acad. Sci. U.S.A., 99 (26), 16999-16903 (2002)
                                                           BC037782 Septemberical protein LOC148206, mRNA (cDNA clone NACE:4797729), with apparent retained intron.
                                                                                                                                                                                                                                                                                                                          Sukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Suteleostomi;
Mammalia; Sutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 2698)

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Direct Submission
Submitted (16-SEF-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                BC037782.1 GI:23349076
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                                                                                                                                                                                                                                                              Homo sapiens (human)
                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                             BC037782
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KEYWORDS
SOURCE
ORGANISM
                                                                                          DEFINITION
RESULT 11
BC037782
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TITLE
JOURNAL
                                                                                                                                                             ACCESSION
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USAN

CONTACT: MGC help deek

CONTACT: MGC help deek

CONTACT: MGC help deek

Email: Gappbe-remail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki

TOSHIYUki and Piero Carninoi (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Genome Sequence Centre,

BC Canada

info@bcgsc.bc.ca

Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,

Susanna Chan, Readman Chiu, Chris Fjell, Brin Garland, Ran Guin,

Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo

Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven

Ness, Pawan Pandoh, Anna Lisa Prabhu, Parvaneh Saeedi, Jacqueline

Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,

Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,

George Yang, Scott Zuyderduyn, Marco Marra.
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 70 Row: g Column: 16
This clone was selected for full length sequencing because it
passed the following selection criteria: Similarity but not
                                                                                                                                                                                        identity to protein
This clone has the following problem: retained intron.
Location/Qualifiers
1. 2698 "...-. ....innians"
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source
FEATURES
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1396 pargretrecacerracracataradargarrearacragagagaaaceracaaa 1455
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2253)
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                                                                                                                                                                                                                                                                                                                                                                    7 GAAAGTGACGAAACCAAATCGATATCATCTTTAATATCTTCTTCTTCTTCATCACGTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       187 GATAAAGCATTTTTCAGAAAATCACATTTGGAAACACATATTGTATCACATTCCGGAAAAA
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                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                    tch 7.3%; Score 90.4; DB 11; Length 2698; al Similarity 51.8%; Pred. No. 4.1e-07; 258; Conservative 0; Mismatches 231; Indels 9;
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Contact: MGC help desk
Email: cgapbs-römail.nih.gov
Iissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
                                                                                    hypothalamus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2253 bp mRNA
Mus musculus, clone IMAGE:3674739, mRNA.
BC028252
                                                                              /tissue type="Brain, hypotha
/clone lib="NIH MGC 96"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1516 CATACTGGAGAGAACCT 1533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         484 CATCATGGTGGATCTCCT 501
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                                                                                                                                                                                                                                                          Query Match
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Matches 25
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KEYWORDS
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Contact: nisc_mcc@nigri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J. Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             be found
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1117 ACACATATAGGAATACATACTGGGGAAAAGCCCTACAAATGTAATCAATGTGATAAAGCC 1176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LIMB at: http://image.llnl.gov Series: IRAK Plate: 65 Row: a Column: 17 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 13386417 This clone has the following problem: frame shifted.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 CCCAAAAAGTATATTTGCACATATGAAGGGTGTGATAAAGCCTATAATCGACCATCATTA 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="Mammary tumor metastatized to lung. Tumor arose spontareously from a senescent normal mammary (clonal) outgrowth infected with the virus MMTV." /clone lib=NCI CGAP_Lu29" /lab_host="NDIDE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  943 GIGCAAACCCATATAAGGATACATACTGGAGAAAACCCTTCAAATGTA----ATCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gatthersburg, Maryland;
Web site: http://www.nisc.nih.gov/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab_host="DH10B"
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/mol type="mRNA"
/strain="CZECH II"
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Matches 256; Conserv
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 604)
Diases 1 to, Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Magai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., G.Yare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: +55-11-2704922
Email: asimpson@ludwig.org.bx
This sequence was derived from the FAPESP/LICR Human Cancer Genome
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
Project./www.ludwig.org.br/scripts/gethtml2.pl?tl=kt2=MR3-HT0446-260
300-201-f06kc3=2000-03-2k/scripts/gethtml2.pl?tl=kt2=MR3-HT0446-260
Seq primer: puc 18 forward
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                                                                                                                                                                                                                                     BE161630 604 bp mRNA linear BST 21-JUN-2000 MR3-HT0446-260300-201-£06 HT0446 Homo sapiens cDNA, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       129 GCAACATTTAAGAACCCACAGTAATGATGGACGGTATAAATGTACAGTGGACGATTGTGA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     162 AAGACATAGGAGAATTCATACTGGAGAGAAAACCGTACAAATGTAAGGT-----TTGTGA 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shotgun sequencing of the human transcriptome with ORF expressed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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AAACATACTGGAG 1309
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Matches 23
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Rlauener, R.D., Collins, F.S., Wagner, L., Schemen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Staplecon, M., Soares, W.M. B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Abramson, R.D., Mullahy, S.J., Bonaldo, N.B., Peters, G.J.,
McKernan, K.J., Mallah, Y.S., J., Boack, S.A., McEwan, P.J.,
Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whithig, M., Madan, A., Young, A.C., Shevchenko, Y.,
Butterfield, Y.S., Kazywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse conv. Sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BC032590 3609 bp mRNA linear HTC 19-NOV-2003 Homo sapiens cDNA clone IMAGE:5502691, containing frame-shift
249 ACCATTCCATTGTTCAGTGTGTGTAAAGGGGTTAATTCTCGACAACACTTGAAAAGACA 308
                                                                                                     309 TGAAATCACCCATAC---AAAGTCATTTAAATGTACATTTGAAAATTGTCAAGAAGCATT 365
                                                                                                                                                          366 ITATAAACATCATTAAGACATCATATATTATCTGTTCATGAAAAACATTAACGTG 425
                                                                                                                                                                                                                                                                   396 TCACAAATCAAACCTTGCATGTCATCATAGACTTCATACTGGAGAAACCTTACAAGTG 455
                                                                                                                                                                                                                                                                                                                          426 TAAACAATGTAATAAAGTTTTCACTCGACCTTCAAAATTAGCACAACATAAATTAAAACA 485
                                                                                                                                                                                                                                                                                                                                                                            456 TAATGAATGIGGCAAGGITITITAATIGAAATCAAACCITGAACATCATAGAGITCA 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 3609)

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Submitted (06-20N-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genemics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                 276 ACCTTACAAGTGTAATGAGTGTGGCAAGACCTTTGTTCAAAATTCATCTTGTAATGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
TONA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BC032590.1 GI:21619671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    516 TATCGGAGAAAAACCT 531
                                                                                                                                                                                                                                                                                                                                                                                                                                486 TCATGGTGGATCTCCT 501
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Homo sapiens
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SOURCE
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AUTHORS
TITLE
JOURNAL
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PUBMED
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COMMENT
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Contact: nisc mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,K.W., Bouffard,G.G., Breen,K., Brinklay,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho.S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                           Clone distribution: MGC clone distribution information can be found through the I.M. AG. E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 69 Row: g Column: 20 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 13430873 This clone has the following problem: frame shifted.
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AL705393.1 GI:19688748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      426 TAAACAATGTAATAAAGTTTTCACTCGACCTTCAAAATTAGCACAACATAAATTAAAACA 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69 AAAGTATATTTGCACATATGAAGGGTGTGATAAAGCCTATAATCGACCATCATTATTAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue type="Eye, retinoblastoma"
/clone_lib="NIH_MGC_67"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pCMV-SPORT6"
Web site: http://www.nisc.nih.gov/
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/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5502691"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1001 TATCGGAGAAAACCT 1016
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This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKE?), Email s.wiemann@dkfz-heidelberg.de;
sequenced by MediGenomix (Martinsried/Germany) within the cDNA
sequencing consortium of the German Genome Project. No s1 sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 ACCICCCAAAAAGTATATTTGCACATATGAAGGGTGTGATAAAAGCCTATAATCGACCATC 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86 ACATACTGGAAAGAATCTTTCAAATGTAAAGAATGTGAAAAGTCATTTTGCATGCTTTC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 ATTAITAGAGCAACATTTAAGAACCCACAGTAATGATCGACCGTATAAATGTACAGTGGA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        146 ACACTTAGCTCAACATAAAAAATTCATAGTGGAGAAACCCTACAAATGTAAA---- 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 CGATICIGATAAAGCATTITCAGAAAATCACATTIGGAAACACATATTGTATCACATTC 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             201 -GAATGTGGGAAAGCCTATAATGACACCTCAAACCTTTCTACACATAAAAAAATTCATAC 259
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                                                    Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 535)
Ottenwaelder, B., Obermaier, B., Mewes, W., Mewes, H.W., Weil, B. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /dev_stage="adult"
/lab_host="BH10B"
/clone_lib="68f (synonym: hlcc3)"
cDNA-collection"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This clone (DXFZp686M1835) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin- Charlottenburg, GERMANY; Email: clone@rzpd.de. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9; Gaps
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7.2%; Score 88.6; DB 9; Length 535;
Best Local Similarity 53.3%; Pred. No. 1.1e-06;
Matches 237; Conservative 0; Mismatches 199; Indels
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp686M1835"
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                              Homo sapiens (human)
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Contact: MIPS
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EST (Ottenw
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Search completed: May 9, 2004, 10:57:43 Job time : 3623.38 secs

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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

5, 2004, 15:14:51; Search time 58 Seconds (without alignments) 2007.062 Million cell updates/sec Run on:

US-09-831-804-3 Title: Perfect score:

1 MSESDETKSISSLISSSSSS......PLVKKARMDLLPNETSVISR 412 Sequence:

Scoring table:

1586107 seqs, 282547505 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A Geneseq 29Jan04:* L: geneseqp1980s:* P: geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* 4 70 0 7 8 Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STRAMMITES

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9 Drosophil 2 TRAF6-inh 4 Human nuc 4 Human MDD 10 Human KDD 10 Human KDD 10 Novel hum 10 Novel hum 11 Novel hum 12 Human nuc 16 Novel hum 16 Novel hum 17 Human nuc 18 Human pol 18 Human pol 18 Human prol 18 Huma	Human Human Human Human
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	376 376 376 376
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ALIGNMENTS

Transcription factor; CATFILIA; DNA-binding protein; ribosomal RNA 5S gene; fungal infection. A transcription factor designated CATFIIIA. AAY93316 standard; protein; 412 AA. 04-SEP-2000 (first entry) Candida albicans. AAY93316; AAY93316

Misc-difference 339 /note= "Ser encoded by CTG" /note= "Ser encoded by CTG" Location/Qualifiers Misc-difference 193

WO200028037-A1. 18-MAY-2000,

98FR-00014147. 99WO-FR002739. 10-NOV-1998; 09-NOV-1999;

Camier S, Sentenac A; (HMRI) HOECHST MARION ROUSSEL WPI; 2000-376549/32. Bordon-Pallier F,

N-PSDB; AAA15398.

New nucleic acid encoding Candida albicans transcription factor, useful e.g. in screening for antimycotic agents and for immunization.

Claim 12; Page 35-36; 45pp; French.

The present sequence represents a Candida albicans transcription factor, designated CATFILIA. The polypeptide is a DNA-binding protein, which is involved in initiating transcription of the ribosomal RNA 5S gene. The polymucleotide is used to screen for its specific inhibitors, potentially useful as antimycotic agents, to raise an antibody response that is protective against fungal infection and to raise antimycotics. Such antibodies, as well as the polypeptides and polynucleotides are used in

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compositions for diagnosing and treating fungal infections, e.g. by detecting polymorphisms and mutations
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signal transduction; DNA replication; cell division; growth;
proliferation; Candida albicans; fungicide; antifungal.
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                                                                                                                 DB 3; Length 412;
                                                                                                            100.0%; Score 2229; DB 3; Length 4 100.0%; Pred. No. 1e-167; ive 0; Mismatches 0; Indels
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                                                                                                                                                        Matches 412; Conservative
                                                                                                                               Similarity
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                                                                  Sequence 412 AA;
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Constructing strains for identifying gene products as effective targets for therapeutic intervention, by inactivating in the strain one allele of
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                                                                                                                                                                        29-DEC-2000; 2000US-0259128P.
20-FEB-2001; 2001US-00792024.
22-AUG-2001; 2001US-0314050P.
                                                                                                                                                                                                        (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                       WPI; 2002-566694/60.
N-PSDB; ABZ32206.
                                                                                                                                                                                                                        Roemer T, Jiang B,
RESULT 2
        ABP73656
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The invention relates to constructing (MI) a strain of diploid fungal cells in which both alleles of a gene are modified, comprising modifying cone allele by insertion or replacement by a cassette having an expressible selectable marker and modifying other allele by recombination, of a promoter replacement fragment with a heterologous promoter, so that expression of the second allele is regulated by the promoter. (MI) is useful for constructing a strain of diploid fungal cells in which both alleles of a gene are modified. The diploid fungal cells having both alleles of a gene are modified. The diploid fungal cells having both alleles of a gene are modified. The diploid fungal cells having both alleles and/or pathogenicity of a fungus, a gene that is essential to the survival or growth of a fungus, a gene that contributes to the vivilence and/or pathogenicity of a fungus on antifungal agent that inhibits the growth of a fungus on antifungal agent that inhibits the growth of a fungus on antifungal activity of a gene product, preferably enzymatic activity, carbon disease. (MI) is useful for identifying a compound which modulates the compound extebolism, biosynthetic, transporter, transferiblional, transporter, biosynthetic, transporter, transferiblional, transduction, DNA replication and cell division activity. The method is useful for identifying a compound having the activity. The method is useful for identifying a compound having the activity. The method is useful for identifying a compound having the seemial Candida albicans protein used in the method of the invention.

Note: The sequence date for this parter is not represented in the printed specification but is based on sequence information supplied to Derwent by the bropsen patent Office
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a gene and placing other allele of the gene under conditional expression
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                                                   Claim 44; SEQ ID NO 7493; 167pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 99.8%; Score 2225; DB 5; Best Local Similarity 99.8%; Pred. No. 2.1e-167; Matches 411; Conservative 1; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 412 AA;
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The invention relates to novel purified or isolated nucleic acids of essential genes of Aapergillus funigatus. The isolated nucleic acids of the invention are used to treat or prevent infectious by a pathogenic organism such as A. funigatus, to treat a non-infectious disease in a subject (e.g. cancer), to prevent or contain contamination of an object by A. funigatus, or prevent or inhibit formation on a surface of a choistilm comprising A. funigatus. The polynucleotides are useful for expressing recombinant protein for characterisation, screening or therapeutic use, as markers for host tissues in which the pathogenic corganisms invade or reside, for comparing with the DNA sequence of A. funigatus to identify duplicated genes or paralogues having the same or corganism invade or reside, for comparing with the DNA sequence of A. funigatus to identify duplicated genes or paralogues having the same or similar biochemical activity and/or function, for comparing with DNA sequences of other related or distant pathogenic organisms to identify potential orthologous essential or virulence genes, for selecting and of expression patterns, for ratising anti-protein antibodies, as an expension of expression patterns, for ratising anti-protein antibodies, as an exter for cresponse, and for identifying polymucleotides encoding the other protein cuttingen to raise anti-DNA antibodies or to elicit another immune course or to identify inhibitors of the binding course or to identify inhibitors of the binding course or to identify inhibitors of the case or to cetermine levels of the protein in biological linds, as a marker for checking in which pathogenic organism invade or reside, and to electer correlative receptors or ligands in the case or virulence of acceptors. This sequence represents a processing in the easential genes or the seminary of another fundamental organisms.
                                                    Fungicide; cytostatic; essential gene; Aspergillus fumigatus; infection; cancer; contamination; biofilm; antibody; immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New purified or isolated nucleic acids of essential genes of Aspergillus fumigatus, useful for treating or preventing infections by A. fumigatus, or for treating a non-infectious disease in a subject e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jiang B, Tishkoff D, Zamudio C, Eroshkin AM, Hu W, Lemieux SM;
Aspergillus fumigatus essential gene protein #313.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure, Page, 175pp, English,
                                                                                                                                                                                                                                                                                                                                 23-APR-2001; 2001US-0285697P.
27-APR-2001; 2001US-0287066F.
05-UUN-2001; 2001US-02990P.
09-UUL-2001; 2001US-031899P.
31-AUG-2001; 2001US-0316362P.
                                                                                                                                                                                                                                                                                  23-APR-2002; 2002WO-US013142.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ELIT -) ELITRA PHARM INC.
                                                                                                                           Aspergillus fumigatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-093124/08.
                                                                                                                                                                               WO200286090-A2.
                                                                                                                                                                                                                                 31-0CT-2002
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Sequence 564 AA;

Aspergillus fumigatus of the invention

21; 20 14 ISSSSSRP---KKYICTYEGCDKAYNRPSLLEQHLRTHSNDRPYKCTVDDCDKAPFRKS 20.0%; Score 445; DB 6; Length 564; ilarity 30.3%; Pred, No. 1.8e-26; Conservative 62; Mismatches 164; Indels 62; Gaps Similarity Local Simi Query Match Matches ò

130 71 HLETHIVS-HSEKKPFHCS--VCGKGVNSRQHLXRHEITH--TKSFKCT-PENCQEAFYK 124 ISTISAKYPSELKTHRCPFDGCTKAFNRPARLQEHLRSHNNERIFKCTFEECDKTFLRAS

g ð 셤

- HQSLRHHILSVH--EKTLTC-----KQCNKVFTRPSKLAQHKLKHHGGSPAYQCDH- 173

174 ----PGCFKNFQTWSVLQFHIKQSHPKLKCPKCGKGCVGKKGLSSHM-LSHDDSTM--IK 226 250 SQHAEGAEATFPTYALLQAHIRSVHPP-QCPNCALTCATSRELRRHLEVAHGDVSLEERK 308 309 IFPCTVPGCD-RSFTKKGNLTVHIRTVHQGERRFVCGETDLSSSKKVSGWNN--DNGCGK 365 418 276 --GSKLMNLHELETEKLKVEEDEEDSL----DEKRSDVRSDSMSAQRSIKSFTASLE 329 227 IWTCDY--CDVGKFAKKNELVEHYNIFHDGNI-----PDDLLKETEVKKLENLLDQ----366 RYGSKLALEEHIRTAHLGYQNAKAERRQRLGITRDRQHSTATSPGVSA-----LAALT GSKSVSKLISNSGKKINCPKNNCDRMFSREYDLRRHL--KWHDDNLQRIESFL 380 | : | : | : | | GEGYAEE----TGRHIACLVESCPHRFHRDYDLWVHMSGKHHFSEEETRDLFL 467 419 음 유 엄 ઠે ò ò ò 셤

Ą. ABJ26255 standard; protein; 564

ABJ26255;

(first entry) 16-APR-2003

Aspergillus fumigatus essential gene protein #913.

Fungicide; cytostatic; essential gene; Aspergillus fumigatus; infection; cancer; contamination; biofilm; antibody; immune response.

Aspergillus fumigatus.

WO200286090-A2.

31-OCT-2002

23-APR-2002; 2002WO-US013142.

27-APR-2001; 2001US-0287066P. 05-JUN-2001; 2001US-0295890P. 09-JUL-2001; 2001US-0303899P. 23-APR-2001; 2001US-0285697P

31-AUG-2001; 2001US-0316362P.

(ELIT-) ELITRA PHARM INC

Lemieux SM; Hu W, Eroshkin AM, Zamudio C, Tishkoff D, Jiang B,

WPI; 2003-093124/08.

New purified or isolated nucleic acids of essential genes of Aspergillus fumigatus, useful for treating or preventing infections by A. fumigatus, or for treating a non-infectious disease in a subject e.g. cancer.

Disclosure; Page; 175pp; English.

The invention relates to novel purified or isolated nucleic acids of the essential genes of Aspergillus fundatus. The isolated nucleic acids of the invention are used to treat or prevent infections by a pathogenic organism such as A. fundatus, to treat a non-infectious disease in a subject (e.g. cancer), to prevent or contain contamination of an object by A. fundatus, or to prevent or contain contamination of an object expressing recombinant protein for characterisation, screening or expressing recombinant protein for characterisation, screening or therapeutic use, as markers for host tissues in which the pathogenic organisms invade or reside, for comparing with the DNA sequence of A. fumigatus to identify duplicated genes or paralogues having the same or similar biochemical activity and/or function, for comparing with DNA sequences of other related or distant pathogenic organisms to identify potential orthologous essential or virulence genes, for selecting and

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making oligomers for attachment to a nucleic acid array for examination of expression patterns, for raising anti-protein antibodies, as an antigen to raise anti-DNA antibodies or to elicit another immune response, and for identifying polymucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction. The polypeptides may be used to raise antibodies or to determine levels of the protein in biological fluids, as a marker for host tissues in which pathogenic organism invade or reside, and to isolate correlative receptors or ligands in the case or virulence factors. This sequence represents a protein of one of the essential genes of Aspergillus fumigatus of the invention
      8X88888888888888888
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Sequence 564 AA;

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21;
                                                                                                                                         71 ISTISAKYPSELKTHRCPFDGCTKAFNRPARLOGHLRSHNNERIFKCTFEECDKTFLRAS 130
                                                                                                                                                                                                                HLETHIVS-HSEKKPFHCS--VCGKGVNSRQHLKRHEITH--TKSFKCT-FENCQEAFYK 124
                                                                                                                                                                                                                                                                131 HINHHIKSAHTGVRDYVCDRPGCGKSFVTGSRLRRHLAAHDGRDKYRCTEYPPCNETFRK 190
                                                                                                                                                                                                                                                                                                                    HOSLRHHILSVH--EXTLTC-----KOCNKVFTRPSKLAQHKLKHHGGSPAYQCDH- 173
                                                                                                                                                                                                                                                                                                                                                                       HSTLOKHIMTAHLKOKPFOCPHTDPSTGGKCTMAFDTAGHLRAHESRIH-TEKRFSCTEC 249
                                                                                                                                                                                                                                                                                                                                                                                                                           174 ----PGCFKNFQTWSVLQFHIKQSHPKLKCPKCGKGCVGKKGLSSHM-LSHDDSTM--IK 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                250 SQHAEGAEATFPTYALLQAHIRSVHPP-QCPNCALTCATSRELRRHLEVAHGDVSLEERK 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IWICDY---CDVGKFAKKNELVEHYNIFHDGNI-----PDDLLKETEVKKLENLLDQ---- 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        309 IFPCTVPGCD-RSFTKKGNLTVHIRTVHQGEKRFVCGETDLSSSKKVSGWNN--DNGCGK 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           276 --GSKLNNLHELBTEKLKVEEDEEDEL----DEKRSDVRSDSMSAQRSIKSFTASLE 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RYGSKLALEEHIRTAHLGYQNAKAERRQRLGITRDRQHSTATSPGVSA-----LAALT 418
                                                                                                      14 ISSSSSRP---KKYICTYEGCDKAYNRPSLLEQHLRTHSNDRPYKCTVDDCDKAFFRKS 70
20.0%; Score 445; DB 6; Length 564;
30.3%; Pred. No. 1.8e-26;
.ive 62; Mismatches 164; Indels 62; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  330 GSKSVSKLISNSGKKINCPKNNCDRMFSRBYDLRRHL--KWHDDNLQRIESFL 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GEGYAEE ----TGRHIACLVESCPHRFHRDYDLWVHMSGKHHFSEEETRDLFL 467
                      Best Local Similarity 30.3 Matches 125; Conservative
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Human; chromosome mapping; gene mapping; gene therapy; forensic food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                Novel human diagnostic protein #390.
                  ABG00399 standard; protein; 1212 AA
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23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                              30-MAR-2001; 2001WO-US008631.
                                                            (first entry)
                                                                                                                                                                                                                                                 (HYSE-) HYSEQ INC
                                                                                                                                                      WO200175067-A2.
                                                                                                                                   Homo sapiens.
                                                            13-FEB-2002
                                                                                                                                                                          11-0CT-2001,
           ABG00399
RESULT
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AAU30831 standard; protein; 1230 AA

AAU3 083

8XXX

(first entry)

18-DEC-2001

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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed crivity is useful in gene therapy techniques to restore normal crivity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in issue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for generation end products dependent on DNA and and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic maino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the printed specification, but was obtained in the way and the printed specification, but was obtained in the printed specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18.7%; Score 416.5; DB 4; Length 1212;
32.6%; Pred. No. 9.1e-24;
.ive 45; Mismatches 148; Indels 47; Gaps ·15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      975 EKPYKCEECGKAFNRSSKL/THKIIHTGEKP-YKCEE--CGKAFISSSTLNGH-KRIHTR 1030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEKKPFHCSVCGKGVNSRQHLKRHEITHT--KSFKCTFENCQEAFYKHQSL-RHHILSVH 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  137 EKTLICKQCNKVFTRPSKLAQHKLKHHGGSPAYQCDHPGCFKNFQTWSVLQFHIKQSHPK 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      197 ---LKCPKCGKGCVGKKGLSSHMLSHDDSTMIKIWTCDYCDVGKFAKKNELVEHYNIFHD 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          254 GNIPDDLLKETEVKKLENLLDQGSKLNNLHELETEKLKVEEDEEDEEDSLDEKRSDVRSD 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1124 PYKYKECGKSFNRSSTFTK--HKVIHTGVKLYKC--BECGKSFFWSSALTRHKKIH 1175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            861 TREKTYKC--EECGKAFSQPSHLTTHKRMHTGEKPYKC--EECGKAFSQSSTLTTHKIIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 SRPKKYICTYEGCDKAYNRPSILEQHIRTHSNDRPYKCTVDDCDKAFFRKSHLETHIVSH
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                                                                                                                                                New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                               Claim 20; SEQ ID NO 30758; 103pp; English.
                        Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 32.68
Matches 116; Conservative
                           Liu C,
                                                                          WPI; 2001-639362/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1212 AA;
                                                                                                      N-PSDB; AAS64586
                                                                                                                                                                                                                                biodiversity.
                           Drmanac RT,
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311 RSDSMSAQRSIKSFTASLEGSKSVSKLISNSGKKINCPKNNCDRMFSREYDLRRHLKWH 369
                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                    22-OCT-2001
                                                                                                                                                                                                                                                                                                                       26-JUL-2001
                                                                                                                                                                                                                                               leukaemia.
                                                                                                             AAM38689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tang YT,
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Zhou P,
                                                               RESULT 7
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                                                                                                                                                                                                                                                                                                                                                        The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the present of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and artagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the proteins concluding the polypeptides and calls genetically engineered to express them are also useful for producing the proteins. The proteins are nutritional aupplements. They may be used to soliferation; to regulate haematopoiesis; and in bone, cartilage, tendon profession, as antitianglammatory agents; and in treatment of leukaemias. ANU29510-AAU3304 represent the amino acid sequences of novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              947 IGBKPYKCEECGKAFRKSSTLTEHKIIHTGEKPYKC--BECGKAFSQSSTLTRHTRWHTG 1004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 SEKKPFHCSVCGKGVNSRQHLKRHEITHT--KSFKCTFENCQEAFYKHQSL-RHHILSVH 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EKTLICKOCNKVFTRPSKLAQHKLKHHGGSPAYQCDHPGCFKNFQTWSVLQFHIKQSHPK 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79
                                                                                                                                                                                                                                                                                               Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TREKPYKC--EECGKAFSQPSHLTTHKRMHTGEKPYKC--EECGKAFSQSSTLTTHKIIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 SRPKKYICTYEGCDKAYNRPSLLEQHLRTHSNDRPYKCTVDDCDKAFFRKSHLETHIVSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         197 LKCPKCGKGCVGK-----KGLSSHMLSHDDSTMIKIWTCDYCDVGKFAKKNELVEHYNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18.1%; Score 403; DB 4; Length 1230; 32.9%; Pred. No. 1.16-22; Live 45; Mismatches 144; Indels 52; Gaps
                                                  stem cell proliferation, haematopoiesis, nerve tissue regeneration,
immune suppression, immune stimulation, anti-inflammatory, leukaemia
                                         gene therapy; nutritional supplement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 20; Page 355; 765pp; English.
                  Novel human secreted protein #1322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            secreted proteins of the invention
                                                                                                                                                              16-APR-2001; 2001WO-US008656.
                                                                                                                                                                                                                                                  Liu C, Drmanac RT;
                                                                                                                                                                                      18-APR-2000; 2000US-00552929
                                                                                                                                                                                                 26-JAN-2001; 2001US-00770160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 32.99
Matches 118; Conservative
                                                                                                                                                                                                                                                                          WPI; 2001-611725/70.
                                        vaccination;
                                                                                                                                                                                                                         (HYSE-) HYSEQ INC.
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                                                                                                              WO200179449-A2
                                                                                        Homo sapiens
                                                                                                                                      25-OCT-2001
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                                                                                                                                                                                                                                                  lang YT,
                                         Human;
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encoded polypeptides (AAM)8642-AAM42213) with nootropic, decoded polypeptides (AAM)8642-AAM42213) with nootropic, minucosuppressant and cyrostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system, such as peripheral nervous injuries, peripheral nervous alcalised neuropathies and central nervous system diseases, such as alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as Immune system suppression, activity, chemotactic/chemokinetic activity, heamostatic and therapy, drug screening, assays for receptor activity, architics and inflammation, leukamenias and assays for receptor activity, arthritis and inflammation.
1152 REKPYKYKECGKSFNRSSTFTK--HKVIHTGVKLYKC--BECGKSFFWSSALTRHKKIH 1206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wang D;
Zhao QA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          s disorders. Note: The sequence data for this patent did not form of the printed specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, nootropic, immunosuppressant; cytostatic; gene therapy; cancer peripheral nervous system; CNS; Alzheher's; Parkinson's disease; Huntington's disease; hameingten's disease; hameington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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Zhang J,
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Yang Y,
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Xue AJ,
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Wang Z, Wehrman T, Xu C,
Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                          Human polypeptide SEQ ID NO 1834.
                                                                                                                                                                                                         AAM38689 standard; protein; 809
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21-JAN-2000; 2000US-00488725.
25-APR-2000; 2000US-0055217.
20-UJN-2000; 2000US-00596042.
19-UJL-2000; 2000US-00620312.
03-MJG-2000; 2000US-0063450.
14-SEP-2000; 2000US-0063450.
19-CT-2000; 2000US-0063914.
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121;
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Matches 121
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                                                                                                                                                                                                                  176
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                                                                                                                                                                                                                                                                                          FKNFQTWSVLQFH -- IKQSHPKLKCPKCGKGCVGKKGLSSHMLSHDDSTMIKIWTCDYCD 234
                                                                    59
                                                                                          TECGEAFSRSSNLTKHKKIHTEKKPYKC--EECGKAFKWSSKLTEHKLTHTGEKPYKC--
                                                                                                                                                                                                                                                                                                                                                                                            DDCDKAFFRKSHLETHIVSHSEKKPFHCSVCGKGVNSRQHLKRHEITHT--KSFKCTFEN
                                                                                                                                                                            EEGGKAFNWPSTLTKHNRIHTGEKPYKCEVCGKAFNQFSNLTTHKRIHTAEKPYKC--EE
                                                                                                                                                                                                                  CQEAFYKHQSL-RHHILSVHEKTLTCKQCNKVFTRPSKLAQHKLKHHGGSPAYQCDHPGC
                                                                                                                                                                                                                                                  CGKAFSRSSNLTKHKKIHIEKKPYKCEECGKAFKWSSKLTEHKITHTGEKP-YKCEE--C
                                                                                                                                                                                                                                                                                                                              GKAFNHFSILTKHKRIHTGEKPYKCEECGKAFTQSSNLTTHKKIH----TGEKFYKCEEC-
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                                                                  SESDETKSISSLISSSSS--SRPKKYICTYEGCDKAYNRPSLLEQHLRTHSNDRPYKCTV
                                Gaps
                              34;
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Emerling
Pred. No. 1.1e-22;
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Sprague WW,
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Richardson TW, Lee EA,
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                            53;
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2001US-032270P.
2001US-0324040P.
2001US-0326732P.
2001US-0346716P.
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          31.9%;
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                                121; Conservative
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Matches 121; Conserv
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14-SEP-2001; 2
21-SEP-2001; 3
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19-OCT-2001;
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Becha SD,
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The invention describes a novel human isolated nucleic acid-associated polypeptide (NAAP). The polypeptides and polynucleotides are useful in diagnosing, treating and preventing diseases or conditions associated with the decreased expression or overexpression of NAAP, such as cell proliferative (e.g. cancer, atherosolarosis), neurological (e.g. proliferative (e.g. cancer, atherosolarosis), neurological (e.g. allergies) and developmental (e.g. Hypothyroidism, Cushing's syndrome) alsorders, or infections. These are also useful in assessing the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of NAAP. The NAAP or its fragments are useful in screening compounds for effectiveness as agonist or antagonist of the polypeptides, or in altering the expression of the target polynucleotide and compounds for in altering the expression of the activity of the polypeptide. The microarray is useful in monitoring or measuring protein-protein interactions, drug-target interactions, and gene expression profiles. This is the amino acid sequence of a novel human nucleic acid-associated
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                                                                                                                                                                                                                                                                                                                                                                     New human nucleic acid associated proteins (NAAP), useful for diagnosing, treating and preventing diseases or conditions associated with the aberrant NAAP expression e.g. cancer, AIDS, atherosclerosis, epilepsy, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              421
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                                               Ison CH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           310 EKPYKCEECGKAFSQSSTLTTHKI-IHTGEKFYKCEE--CGKAFSQLSHLTTHKRIHSGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SRPKKYICTYEGCDKAYNRPSLLEQHLRTHSNDRPYKCTVDDCDKAFFRKSHLETHIVSH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             255 NIPDDLLKETEVKKLENLLDQGSKLNNLHELETEKLKVEEDEEDBEDSLDEKRSDVRSDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EKP---YKCEECGKAFNLSSQLTTHKIIHTGE-KPYKCEEC------GKAFNQSST
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Thangavelu K, Warren BA, Tran UK, Yue H, Xu Y, Yue H, Li JX; Hafalia AJA, Sanjanwala B, Marquis JP, Gorvad AE, Lee SY, Iso Baughn WR, Chawlala NK, Nguyen DB, Swarnakar A, Zebarjadian Y, Thornton M, Yao MG, Khan FA, Gandhi AR, Yang J, Kable AE; Burford N, Ramkumar J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LRRHLKWHD--------BNLQRIESFLNSIEKEE 387
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htfill. The polypeptide is probabaly a DNA-binding protein probably involved in initiating transcription of the gene for ribosomal RNA 55 and mantaining the stability of transcription of other control genes. The htfillA polynucleotides and polypeptides are used to make therapeutic or diagnostic compositions for diseases associated with disorders of transcriptional control, particularly cancer or other inherited diseases. The htfillA polynucleotide can also be used to detect anomalies in gene transcription, particularly for diagnosis of inherited diseases, studying diseases involving htfillA
                                                                                                    Human, transcription factor, htfIIIA, DNA-binding protein, transcription, ribosomal RNA 5S gene; transcriptional control, cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PFVCDYEGGGKAFIRDYHLSRHILTHTGEKPFVCAATGCDQKFWIKKSNLKKHFERKHENQ 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 244 DVCRCPREGCGRIYTIVFNIQSHILSFHEES---RPFVCEHAGCGKIFAAKQSLIRH-AV 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      present sequence represents a human transcription factor designated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PYKCTVDDCDKAFFRKSHLETHIVSHSEKKPFHCSV--CGKGVNSRQHLKRH-BITH---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129 QKQYICSFEDČKKTFKKHQQLKIHQCQHTNEPLFKČTQEGCGKHFASPSKLKRHAKAHEĞ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --LKCPK--CGKGCVGKKGLSSHMLS-HDDSTMIKIWTCDYCDVGK-PAKKNELVEHYNI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           165 GSPAYQCDHPGCFKNFQTWSVLQFHIKQSHPK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid encoding human transcription factor IIIA, useful for treatment and diagnosis of cancer and inherited disease.
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ESVSSLTIADAFIAAGESSAPTPPRPALPRRFICSFPDCSANYSKAWKLDAHLCKHTGER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96;
                                                                   A human transcription factor designated htfIIIA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 10; Page 40-41; 49pp; French.
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les 99; Conservative
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N-PSDB; AAA15405.
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                                                                                                                                                                                                                                                                                          10-NOV-1998;
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                                                                                                                                                       Homo sapiens
                                  04-SEP-2000
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AAY93317;
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cancer-associated nucleic acid molecules (N) and proteins (P), where the cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have expostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expression proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps. P. Additionally, N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. Additional to express the proteins. N and P carcinomas and cancers. Additional to the present invention. N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at the profession of the present for SEQ ID NO:1027
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   108 TKSFKCTFENCOBAPYKHOSLR-HHILSVHEKTLTCKO--CNKVFTRPSKLAQHKLKHHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PYKCTVDDCDKAFFRKSHLETHIVSHSEKKPFHCSV--CGKGVNSRQHLKRH-EITH---
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                                                                                                                                                                  Human; colon cancer; colon cancer antigen; diagnosis; detection;
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                                                                                                                                Human colon cancer antigen protein SEQ ID NO:5945.
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31.1%; Pred. No. 9.6e-23;
tive 54; Mismatches 96;
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                                                                                                                                                                                    colorectal carcinoma; chromosome 13.
                                 AA.
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                                AAG75181 standard; protein; 409
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                                                                                                03-SEP-2001 (first entry)
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Matches 99; Conservative
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052, 7921 and 7922
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N-PSDB; AAH34586.
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                                                              AAG75181;
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RESULT 10
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247 ----YVC-QKGCSFVAKTWTELLKGVRETHKEEILCEVCRKTFKRKDYLKQHMKTHAPER 301
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                                                                                                                  197 -- LKCPK--CGKGCVGKKGLSSHMLS-HDDSTMIKIWTCDYCDVGK-FAKKNELVEHYNI
                                                                                       108 TKSFKCTFENCQEAFYKHQSLR-HHILSVHEKTLTCKQ--CNKVFTRPSKLAQHKLKHHG
                                                                                                                                                                                                      165 GSPAYQCDHPGCFKNFQTWSVLQFHIKQSHPK------
                                                                                                                                                                                                                                                                                                                                                                                                                                   251 FHDGNIPDDLLKETEVKK 268
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N-PSDB; AAK52080.
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Ma Y, Zhao QA, V
Xue AJ, Yang Y,
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                                                                                                                                                      Human, transcription factor-IIIA, hTFIIIA, DNA binding protein, ribosome, zinc finger, diagnostic, probe, transcription control, antitumour,
               196
                                                                                                                           --LKCPK--CGKGCVGKKGLSSHMLS-HDDSTMIKIWTCDYCDVGK-FAKKNELVEHYNI 250
                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŝ
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               GSPAYQCDHPGCFKNFQTWSVLQFHIKQSHPK--
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                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR91305 standard; protein; 423
                                                                                                                                                                                                                                           FHDGNIPDDLLKETEVKK 268
                                                                                                                                                                                                                                                                                              344 VHD---PDKKKMKLKVKK 358
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Best Local Similarity
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The invention relates to polymucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or which may induce production of other cytokines in other cell populations. The polymucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy.
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Wang
                                                                                                              Human, cytokine, cell proliferation, cell differentiation, gene the vaccine, peptide therapy, stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory, cancer; leukaemia; nervous system disorder; arthritis; inflammation.
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Chen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drmanac RT, Asundi V, Zhou P, Xu
Wang D, Wang J, Zhang J, Ren F,
Wejhrman T, Goodrich R;
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AAM78947 standard; protein; 622 AA.
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27-AFR-2000; 2000US-00560875.
19-UUJ-2000; 2000US-00529075.
15-SEP-2000; 2000US-0064936.
15-SEP-2000; 2000US-00663561.
20-CT-2000; 2000US-00693325.
30-NOV-2000; 2000US-00693325.
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Wejhrman T,
                                                                                    Human protein SEQ ID NO 1609.
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54 PYKCTVDDCDKAFFRKSHLETHIVSHSEKKPPHCSV--CGKGVNSRQHLKRH-EITH--- 107

8 KSISSL-----ISSSSSR-----PKKYICTYEGCDKAYNRPSLLEQHLRTHSNDR

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activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAKS2581), 2111 (AAKS2582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication
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                                                                                                                                                                                                                                                                                                      82
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                                                                                                                                                                                                                                                                                                      23 KKYICTYEGCDKAYNRPSLLEQHLRTHSNDRPYKCTVDDCDKAFFRKSHLETHIVSHSEK
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                                                                                                                                                                                                                                                                                                                                                                                               KPFHCSVCGKGVNSRQHLKRHEITHT--KSFKCTFENCQEAFYKHQSLRHH-----
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                                                                                                                                                                                                                                                          92; Gaps
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                                                                                                                                                                                                       Query Match
17.7%; Score 395; DB 4; Length 622;
Best Local Similarity 29.7%; Pred. No. 1.8e-22;
Matches 123; Conservative 42; Mismatches 157; Indels
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27-AFR-2000; 2000US-00560875.
20-UUN-2000; 2000US-00590075.
19-UUL-2000; 2000US-00650325.
01-SEP-2000; 2000US-0065361.
20-CCT-2000; 2000US-00693325.
30-NOV-2000; 2000US-00693325.
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encoded polypeptides (AAM)8121-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The production of other cytokines in other cell populations. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, activity, tissue growth factor activity, haematopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity, and may be useful in the diagnosis and/or inflammation. Note: Records for SEQ ID NO 2110 (AAKS2581), 2111 (AAKS2582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication
                                                                                                                                                                                                                                     Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   324 YVCEECGKAFKYSRILTTHKRIHTGEKPYKCNKCGKAFIASSTLSRHEFIHMGKKHYKCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------HGGSPAYQCDHPGCFKNFQTWSVLQFHIKQSH---PKLKCPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGKGCVGKKGLSSHMLSHDDSTMIKIWTCDYCDVGK-FAKKNELVEHYNIFHDGNIPDDL
                                                                                                                                                                                                                                                                                                                                                                             polynucleotides (AAK51456-AAK53435) and the
                                                 Y;
Wang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92;
                                                 Xu C, Cao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KPFHCSVCGKGVNSRQHLKRHEITHT - - KSFKCTFENCQBAFYKHQSLRHH -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----ILSVH-----EKTLTCKQCNKVFTRPSKLAQHKLKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17.7%; Score 395; DB 4; Length 631; 29.7%; Pred. No. 1.9e-22; ive 42; Mismatches 157; Indels
                                           Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, X
Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F,
Xue AJ, Yang Y, Wejhrman T, Goodrich R;
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                                                                                                                                                                                                                                                                                                                         Claim 20; Page 388; 6221pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 123; Conservative
                                                                                                                                                                                                                                                                                                                                                                                The invention relates to
                                                                                                                                                            WPI; 2001-476283/51.
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(HYSE-) HYSEQ INC.
                                                                                                                                                                                      N-PSDB; AAK53064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 631 AA;
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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal ectivity of (II) as useful in gene therapy techniques to restore normal cusful for generating antibodies against it, detecting or quantitating a useful for generating antibodies against it, detecting or quantitating a useful for generating antibodies against it, detecting or quantitating a usplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymuclectide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic dissorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic maino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the printed specification, but was obtained in the printed specification, but was obtained in the printed specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23 KKYICTYEGCDKAYNRPSLLEQHLRTHSNDRPYKCTVDDCDKAFFRKSHLETHIVSHSEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                      Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17.7%; Score 395; DB 4; Length 632; 29.7%; Pred. No. 1.9e-22; ive 42; Mismatches 157; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 20; SEQ ID NO 48745; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                 Tang YT;
                                                                                                                                                                                                                                  30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                              31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 123; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-639362/73
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                                                                                                                                                                                                                                                                                                                                                 (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAS82573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 632 AA;
                                                                                                                                      WO200175067-A2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      biodiversity.
                                                                                              Homo sapiens.
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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain recombinant production of (II). The polymucleotides are also used and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed activity of (II) are the polymucleotides are also used activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of supplement. (II) and its binding partners are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders of supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders of plypeptide and polymucleotide sequences have applications in diagnostics formsics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess blodiversity and to produce other types of data and products dependent on DNA and and and not appear in the printed specification, but was obtained in electronic format directly from WIPO at the printed specification, but was obtained in the will be printed specification, but was obtained in the printed specification, but was obtained in the printed sequences.
                                 CGKAFVASSTLSKHEIIH---TGKKPYKCEBC--GKAFNQSSSLTKHKKI-HTGEKP--- 492
CGKGCVGKKGLSSHMLSHDDSTMIKIWTCDYCDVGK-FAKKNELVEHYNIFHDGNIPDDL 260
                                                                                     261 LKETEVKKLENLLDQGSKLNNLHELET--EKLKVEEDEEDEEDS---LDEKRSDVRSDSM
                                                                                                                           493 YKCEECGKAFN---QSSSLTKHKKIHTGEKPYKCEECGKAFNOSSTLIKHKKIHTREKPY
                                                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; chromosome mapping; gene mapping; gene therapy; forensic; supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                      SAQRSIKSFTASLEGSKSVSKLISNSGKKINCPKNNCDRMFSREYDLRRHLKWH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 20; SEQ ID NO 47312; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel human diagnostic protein #16944.
                                                                                                                                                                                                                                                                                                                        ABG16953 standard; protein; 719 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAR-2001; 2001WO-US008631.
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23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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N-PSDB; AAS81140.
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      202
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                                                                                                                                                                                                                                                                                  RESULT 15
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83 KPFHCSVCGKGVNSRQHLKRHEITHT--KSFKCTFBNCQEAFYKHQSLRHH-----

-----ILSVH-----EKTLTCKQCNKVFTRPSKLAQHKLKH------325 YVCEECGKAFKYSRILTTHKRIHTGEKPYKCNKCGKAFIASSTLSRHEFIHMGKKHYKCE

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385 ECGKAFIWSSVLTRHKRVHTGEKPYKCEB--CGKAFKYSSTLSSH-KRSHTGEKPYKCEE 441

Sequence 719 AA;

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18;
                                                                                              121 AFYKHOSL-RHILLSVHEKTLICKOCNKVFTRPSKLAOHKLKHHGGSPAYOCD---- 172
                                                                                                                                                                                                                                             173 -----HPG-----CFKNFQTWSVLOFH--IKQSHPKLKCPKCGKGCVGKKG 211
                                                                                                                                                                                                                                                                                                                    280 WSSTLFKHKIIHTGEKPYKCEECGKAFTFSSLFKHKVIHTGEKHYKCEECGKVFSWSSS 339
                                                                                                                                                                                                                                                                                                                                                                                              340 LTTHKAIHAGE---KLYKCEEC--GKAFKWSSRLSEHKRI-HTGEKP---YKCEECGKAF 390
                                                                                                                                                                                                                                                                                                                                                                                                                                             271 NILDQGSKLNNLHELETEK--LKVEEDEEDEDS---LDEKRSDVRSDSMSAQRSIKSFT 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       391 SWV---SVLNKHKKIHAGKKFYKCEECGKDFNQSSHLTTHKRIHTGEKPYKCEECGKAF- 446
                                                                                                                                               61 DCDKAFFRKSHLETHIVSHSEKKPFHCSVCGKGVNSRQHLKRHEITHTKSFKCTFFNCQE 120
                                                                                                                                                                                                                                                                                                                                                                         212 LSSHMLSHDDSTMIKIWTCDYCDVGK-FAKKONELVEHYNIFHDGNIPDDLLKETEVKKLE 270
                                                                      3 ESDETKSISSLISSSS--SSRPKKYICTYEGCDKAYNRPSLLEQHLRTHSNDRPYKCTVD 60
Query Match
17.7%; Score 395; DB 4; Length 719;
Best Local Similarity 30.0%; Pred. No. 2.2e-22;
Matches 121; Conservative 51; Mismatches 174; Indels 58; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      326 ASLEGSKSVSKLISNSCKKINCPKNNCDRMFSREYDLRRHLKWH 369
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17.0	17.0	17.0	17.0	17.0	17.0	17.0	17.0	17.0	16.9		16.8			16.8		16.8		16.7	16.7	16.7	16.7	16.6	16.6	16.6	16.5	16.5	16.5	16.4
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18.4%; Score 410.5; DB 11; Length 634;

Query Match

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LUSUE-TEROM N.A.

A SEQUENCE FROM N.A.

A SIZUAL O., Sasaxi N., Aotsuka S., Shoji T., Ichihara T., Shiohata N.,

A SIZUAL O., Sasaxi N., Aotsuka S., Shoji T., Ichihara T., Shiohata N.,

A Matsumcto K., Hirano M., Sano S., Nomura R., Yoshikawa Y.,

A Reriyama S., Sacoh N., Matsunawa H., Takahashi B., Kataoka S.,

Ruga N., Kuroda A., Satoh I., Kamata K., Takani S., Terashima Y.,

Ruga N., Xumanoto J., Isono Y., Kawai-Ho Y., Sato H., Wakamateu A.,

Ishia S., Yamanoto J., Isono Y., Kawai-Ho Y., Satio K., Nishikawa T.,

Rimura K., Yamanohita H., Matsuno K., Nakamura Y., Sakine M.,

Rimura K., Yamanohita H., Magatsuma M., Murakawa K., Kanehori K.,

A kiwchi H., Kanda K., Waqatsuma M., Murakawa K., Kanehori K.,

A sugano S., Nagahari K., Masulo Y., Nagai T.,

Submitted (Jul-2002) to the EMEL/GenBank/DDBJ databases.

I SUBCLIULAR LOCATION: NUCLEAR (BY SIMILARITY).

B CO: GO: OOOS634; C:nucleus; IEA.

InterPro; IPRO0708; ZIL C212.

BRIATI; SRO0356; ZEC-ZH2; 14.

BRANT; SRO0356; ZEC-ZH2; 14.

B PROSITE; PSO0028 ZINC FINGER C2H2 1; 12.

B PROSITE; PSO0028 ZINC FINGER C2H2 2; 14.

W PROSITE; PSO0129 ZINC FINGER C2H2 2; 14.

W PROSITE; PSO0129 ZINC FINGER C2H2 2; 14.

W PROSITE; PSO0129 ZINC FINGER C2H2 2; 14.

W ZINC-finger.
                                                                                        323 KPYKC--KECGKAFTQSSSLKKHLNLHTGKKPYKC--EECDKSFTEKSTLTTHKRIHTGK 378
                                                                                                                                                   83 KPFHCSVCGKGVNSRQHLKRHEITHT--KSFKCTFBNCQEAFYKHQSLR-HHILSVHEKT 139
                                                                                                                                                                             140 LICKOCNKVFTRPSKLAQHKLKHHGGSPAYQCDHPGCFKNFQTWSVLQFH--IKQSHPKL 197
                                                                                                                                                                                                                                                                            437 YKCKECDKSFILKSSLRTHQIIHTGEKP-YKCNI--CGKSFNQCTNLKTHQRLHTGEKPY 493
                                                                                                                                                                                                                                                                                                                         198 KCPKCGKGCVGKKGLSSHMLSHDDSTMIKIWTCDYCDVGKFAKKNBLVEHYNIFHDGNIP 257
                                                                                                                                                                                                                                                                                                                                                          494 KCKECGKSFHYWSSLKSHQNLHSGE---KPYKCKECD-KSFTEKSTLIKHQRI-HTG--- 545
                                                                                                                                                                                                                                                                                                                                                                                                             258 DDLLKETEVKKLE--NLLDQGSKLNNLHELETEKLKVEEDBEDBEDBLDBKRSDVRSDSM 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                       546 ------KKLYKCNICDK--SFTWCASLKTHK-KFHTGEK--------PY 577
                                                               23 KKYICTYEGCDKAYNRPSLLEQHLRTHSNDRPYKCTVDDCDKAFFRKSHLETHIVSHSEK 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           316 SAORSIKSF -- TASLEGSKSVSKLISNSGKKI-NCPKNNCDRMFSREYDLRRHLKWH 369
                            57; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
il Similarity 32.8%; Pred. No. 2e-19;
117; Conservative 54; Mismatches 129; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      404 AA; 45923 MW; B1B35F62F5DF0007 CRC64;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypotherical protein FLJ40479.
Homo sapiens (Human).
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  Best Local Similarity
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SEQUENCE
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                       Matches
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14;
                                                                                          KPFHCSVCGKGVNSRQHLKRHEITHT - - KSFKCTFENCQEAFYKHQSLRHHILSVH - - EK 138
                                                                                                                                   95 KPYKCEECGKASNSSSKLMEHKRIHTGEKPYKC--EECGKAFSWSSSLTEH-KRIHAGEK 151
                                                                                                                                                                                    139 TLTCKQCNKVFTRPSKLAQHKLKHHGGSPAYQCDHPGCFKNFQTWSVLQFH--1KQSHPK 196
                                                                                                                                                                                                                                                                                197 LKCPKCGKGCVGKKGLSSHMLSHDDSTMIKIWTCDYCDVGK-FAKKNELVEHYNIFHDGN 255
                                                                                                                                                                                                                                                                                                               209 YKCEECGKASNSSSKLMEHKRIH---TGBKPYKCEEC--GKAFSWSSSLTEHKRI-HAGE 262
                                                                                                                                                                                                                                                                                                                                                                               256 IPDDLLKETEVKKLENLLDQGSKLNNLHBLETEKLKVEE-DEEDBEDSLDEKRSDVRSDS 314
                                                                                                                                                                                                                                                                                                                                                                                                                           263 KP---YKCEECGKAFTWSSSFTKHKRIHAAE-KPYKCEECGKGFSTFSILTKHKIIHTGE 318
23 KKYICTYEGCDKAYNRPSLLEQHLRTHSNDRPYKCTVDDCDKAFFRKSHLETHIVSHSEK 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            315 --MSAQRSIKSFTASLEGSKSVSKLISNSGKKINCPKNNCDRMFSREYDLRRHLKWH 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Testicular tumor;
MEDLINE=9806976; PubMed=9406578;
MEDLINE=98069676; PubMed=9406578;
Ogawa T., Poncelet D., Kinoshita Y., Noce T., Takeda M., Kawamoto K.,
Udaqawa K., Lecocq P., Marine J., Martial J., Hosaka M.;
"Enhanced expression in seminoma of human zinc finger genes located on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             319 KRYKCEECGKAF--SWSSILTEHKIIHTGEKPYKC--EECGKAFSKSSLTRHKRIH 371
                         39 KPYKC--EECGKAFNRSSILTKHKIIHTGEKPYKC--EECGKGFSSUSTLNTHKAIHABE
                                                                                                                                                                                                                                  152 PYKCEBCGKAFNRSSILTKHKIIHTGEKP-YKCE--GCGKAFSKVSTLNTHKAIHABEKP
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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GO; GO: 0008237; F: metallopeptidase activity; IEA.

GO; GO: 0008237; F: metallopeptidase activity; IEA.

GO; GO: 0008237; F: metallopeptidase activity; IEA.

GO; GO: 0008208; F: proteclysis and peptidolysis; IEA.

INTERPO: IPRO07087; ZnE CZHZ.

INTERPO: IPRO07086; ZnE CZHZ.

INTERPO: IPRO07086; ZnE CZHZ.

INTERPO: IPRO07086; ZnE CZHZ.

INTERPO: IPRO07086; ZnE CZHZ.

INTERPO: IPRO07086; ZnE CZHZ.

INTERPO: IPRO07086; ZnE CZHZ.

INTERPO: IPRO07086; ZnE CZHZ.

INTERPO: IPRO07086; ZnE CZHZ.

INTERPO: IPRO07086; ZnE CZHZ.

INTERPO: IPROSTIE; PRO042; ZNC FINGER CZHZ.

INTERPO: IPROSTIE; PRO042; ZNC FINGER CZHZ.

INTERPO: IPROSTIE; PRO042; ZNC FINGER CZHZ.

INTERPO: IPROSTIE; PRO0442; ZNC FINGER CZHZ.

INTERPO: IPROSTIE; PRO0442; ZNC FINGER CZHZ.

INTERPO: IPROSTIE; PRO0442; ZNC FINGER CZHZ.

INTERPO: IPROSTIE; PRO0442; ZNC FINGER CZHZ.

INTERPO: IPROSTIE; PRO0442; ZNC FINGER CZHZ.

INTERPO: IPROSTIE; PRO0442; ZNC FINGER CZHZ.
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SEQUENCE 395 AA, 45291 MW; D4E06B54DCEOBF9B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0TN-1998 (TrEMBLrel. 06, Created)
01-UUN-1998 (TrEMBLrel. 06, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cancer Genet. Cytogenet. 100:36-42(1998).
-!- SUBCELULAR LOCATION: NUCLEAR (BY SIMILARITY).
EMBL; D70831; BA24450.1; -
HSSP; P08048; 7ZNF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 395 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zinc-finger protein (Fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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Matches
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19;

17.9%; Score 400; DB 4; Length 404; .larity 33.9%; Pred. No. 6.38-19; Conservative 39; Mismatches 163; Indels 34; Gaps

Query Match Best Local Similarity Matches 121; Conserva

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138 KTLICKQCNKVFTRPSKLAQHKLKHHGGSPAYQCDHPGCFKNFQTWSVLQFH--IKQSHP 195
383 YRFSYLIKH-KTSHTGEKFYKCEECGKGFNWSSALTKHKRIH---TGEKPYKCEEC--GK 436
                                                                                                                                                                                                                                                ...----KMIHTGEKPYKC--EECGKAF 494
                                                                                   238 - PAKKNELVEHYNI FHDGNI PDDLLKETEVKKLENLLDQGSKLNNLHELETEKLKVEEDE 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,
Tashiro H., Yamazaki M., Komiyama M., Sugiyama T., Irie R.,
Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
Kawai-Hio Y., Satto K., Nishikawa T., Kimura K., Yamashita H.
Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
Mutakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A.,
Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A RAWARTI BY SILEAL IN CORPUS CONTROLL BY INDEED A MINITED A LOCATION TO THE SMELL BY SILEAL IN CORPUS CONTROLL BY SEQUENCING PROBLEM BY SIMILARITY).

1. SUDDITICED (OCT-2001) to the EMBL/GenBank/DDBJ databases.

1. SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

1. SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

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1. SUBCELLULAR LOCATION: NUCLEAR LINE ROCATIE; PSSOUGS; KTAB; 1.

1. SUBCELLULAR LOCATION: NUCLEAR LINE RECEITE; PSSOUGS; KTAB; 1.

1. SUBCELLULAR LOCATION: NUCLEAR PROCEIN; ZINC; FINGER CAPA; 1.

1. SUBCELLULAR LOCATION: NUCLEAR PROCEIN; ZINC; FINGER CAPA; 1.

1. SUBCELLULAR LOCATION: NUCLEAR PROCEIN; ZINC; FINGER CAPA; 1.

1. SUBCELLULAR LOCATION: NUCLEAR PROCEIN; ZINC; FINGER CAPA; 1.

1. SUBCELLULAR LOCATION: NUCLEAR PROCEIN; ZINC; FINGER CAPA; 1.

1. SUBCELLULAR LOCATION: NUCLEAR PROCEIN; ZINC; FINGER CAPA; 1.

1. SUBCELLULAR LOCATION: NUCLEAR PROCEIN; ZINC; FINGER CAPA; 1.

1. SUBCELLULAR LOCATION: NUCLEAR PROCEIN; ZINC; FINGER CAPA; 1.

1. SUBCELLULAR LOCATION: NUCLEAR PROCEIN; ZINC; FINGER CAPA; 1.

1. SUBCELLULAR LOCATION: NUCLEAR PROCEIN; ZINC; FINGER CAPA; 1.

1. SUBCELLULAR LOCATION: NUCLEAR PROCEIN; ZINC; FINGER CAPA; 1.

1. SUBCELLULAR LOCATION: NUCLEAR PROCEIN; ZINC; FINGER CAPA; 1.

1. SUBCELLULAR LOCATION: NUCLEAR PROCEIN; ZINC; FINGER CAPA; 1.

1. SUBCELLULAR LOCATION: ZINC; FINGER CAPA; 1.

1. SUBCELLULAR LOCATION: ZINC; FINGER CAPA; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 RPKKYIÇTYEĞÇDKAYNRPSLLEQHLRTHSNDRPYKCTVDDCDKAFFRKSHLETHIVSHS
                                                                                                                                                                                           EDEEDSLDEKRSDVRSDSMSAQRSIKSFTASLEGSKSVSKLISNSGKKINCPKONCDRMF
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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17.6%; Score 392; DB 4; Length 555;
Best Local Similarity 32.5%; Pred. No. 3e-18;
Matches 116; Conservative 45; Mismatches 162; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  555 AA; 64025 MW; 75C246D4820FB920 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein FLJ31444.
Homo sapiens (Human)
                                                                                                                      437 AFNESSNLTTH-KMIHTGEKP---YKCDECGKAFN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     555 AA
                                                                                                                                                                                                                                                     357 SREYDLRRH-----LKWHD 370
                                                                                                                                                                                                                                                                                                                                            : | | : | : | : | 495 NRSSTLTKHKITHTGEKSYKWEE 517
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FYKHQSL-RHHILSVHEKTLTCKOCNKVFTRPSKLAQHKLKHHGGSPAYQCDHPGCFKNF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 QTWSVLQFHIKQSHPK---LKCPKCGKGCVGKKGLSSHMLSHDDSTMIKIWTCDYCDVGK 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         267
                                                                                                                                                                             246
                                                                                                                                                                                                                                                                                                                                                                                       306 EE--CGKAFNQSSNLTRH-KKSHTEEKPYKCEECGKALNRPSTLTIHKIIH---TGEKPY 359
                                                                                                                                                                                                                                       171
                                                                                                                         122
                                                                                                                                                                                                                                                                                        247 YKCKECGKAFKHSSTLTKHKIIHTGEKPYKCKECGKAFNQSSKLTEHK-KIHTGEKPYEC 305
                                                                                                                                                                                                                                                                                                                                            DHPGCFYONFQTWSVLQFHIKQSHPK---LKCPKCGKGCVGKKGLSSHMLSHDDSTMIKIW 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63
                 KKYICTYEGCDKAYNRPSLLEQHLRTHSNDRPYKCTVDDCDKAFFRKSHLETHIVSHSEK 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FNRSSHLTTHRIIHTGEKPYKCEECGKAFNOSSTLTTHKITHAGEKP-YKCEE--CGKAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; BC035579; AAH35579.1; -...

EMBL; BC035579; AAH35579.1; -...

R GO; GO:0006572; C:intracellular; IEA.

GO; GO:0006575; F:nucleic acid binding; IEA.

GO; GO:0006575; F:nucleic acid binding; IEA.

R InterPro; IPRO1099; RRAB.

InterPro; IPRO1099; Zf-C2H2.

IN Pfam; PF01057; Zf-C2H2.

IN Pfam; PF01057; RRAB.

R Pfam; PF01057; RRAB.

R ProDom; PF000060; Zf-C2H2.

R ProDom; PR0000603; Zf-C2H2.

R RNART; SM00349; KRAB; 1.

R RNART; SM00355; ZRE-C2H2; 11.

R RNART; SM00355; ZRE-C2H2; 11.

R RNCSITE; PS50805; KRAB; 1.

R RNCSITE; PS50805; KRAB; 1.

R RNCSITE; PS50805; ZINC_FINGER C2H2_2; 12.

R RNCSITE; PS50805; ZINC_FINGER C2H2_2; 12.

R RNCSITE; RS50805; ZINC_FINGER C2H2_2; 12.

R RNCSITE; RS50805; ZINC_FINGER C2H2_2; 12.

R RNCSITE; RS50805; ZINC_FINGER C2H2_2; 12.
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                                                                                                                                                                 -----YKHOS--LRHHILSVHEKTLTCKOCNKVFTRPSKLAQHKLKHHGGSPAYOC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4; Length 542;
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                                                                                                                            KPFHCSVCGKGVNSRQHLKRHEITHT - - KSFKCTFENCQEAF -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-WAR-2003 (TrEMBLrel. 23, Created)
1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to zinc finger protein 208.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             360 KCEEC--GKAFNQSSKLTKHKKI-HTGEKP 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                          229 TCDYCDVGK-FAKKNELVEHYNIFHDGNIP 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      542
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Best Local Similarity 30.0%
Matches 115; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rissum=Testis;
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17.6%; Score 392; DB 4; Length 644;
32.5%; Pred. No. 3.5e-18;
ive 45; Mismatches 162; Indels 34; Gaps 17;
283 KPYKCEECDKAFNRFSYLTKHKI-IHSGEKSYKCEQ--CGKGFNWSSTLTKHRRIHTGEK 339
                                                                                                                    196 KLKCPKCGKGCVGKKGLSSHMLSHDDSTMIKIWTCDYCDVGKFAKKNELVEHYNIFHDGN 255
                                                                                                                                                                            340 PYKCEECGKAFNVSSHLITHKMIH---TGEKPYKCEEC--GKAFNHSSKLIIHKIIHTGE 394
                                                                                                                                                                                                                                                                                    256 IPDDLLKETEVKKLENLLDQGSKLNNLHELET-EKL-KVERDEEDBEDSLD---EKRSDV 310
                                                                                                                                                                                                                                                                                                                                                                 395 KP---YKCEECGKAFN---QSSNLTKHKIIHTGEKLYKCEECGKAFNRSSNLTTHKRIHT 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        289 RENSYQC--EECDKVFKRFSTLTRHKRVHTGEKPFKC--EECGKAFKHSSTLTTHKMIHT 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   345 GEKPYRCEECGKAFYHSSHLTTHKVIHTGEKPFKC--EECGKAFNHPSALTTHKFIHVKE 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              403 KPYKCEECDKAFNRFSYLTKHKI-IHSGEKSYKCEQ--CGKGFNWSSTLTKHRIHTGEK 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          196 KLKCPKCGKGCVGKKGLSSHMLSHDDSTMIKIWTCDYCDVGKFAKKNELVEHYNIFHDGN 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LISSUBLEARAIN,

Bloecker H., Beecher M., Brandt P., Mewes H.W., Weil B., Wiemann S.;

Lubmitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.

C. - STREELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

REMBL; AL834415; CAD33077.1;

RO; GO:0003674; C:nucleus; IEA.

RO; GO:0003675; F:nucleus; IEA.

RO; GO:0003675; F:nucleus of transcription, DNA-dependent; IEA.

INTERPO: IPR001909; KRAB.

RINTERPO: IPR001909; RAB.

RINTERPO: IPR001909; ZICZ2H2.

RINTERPO: IPR001909; ZICZ2H2.

RINTERPO: IPR001909; ZICZH2.

RINTERPO: IPR001909; ZICZH2.

RINTERPO: IPR001909; ZICZH2.

RINTERPO: IPR001909; ZICZH2.

RINTERPO: IPR001909; ZICZH2.

RINTERPO: IPR001909; ZICZH2.

RINTERPO: IPR001909; ZICZH2.

RINTERPO: IPR001909; ZICZH2.

RINTERPO: IPR001909; ZICZH2.

RINTERPO: IPR001909; ZICZH2.

RINTERPO: IPR001909; ZICZH2.

RINTERPO: IPR001909; ZICZH2.

RINTERPO: IPR001909; ZICZH2.

RINTERPO: IPR001909; ZICZH2.

RINTERPO: IPR001909; ZICZH2.

RINTERPO: IPR001909; ZICZH2.

RINTERPO: IPR001909; ZICZH2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               311 RSDSMSAQRSIKSFTASLEGSKSVSKLISNSGKKINCPKNNCDRMFSREYDLRRHLK 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         449 GEKPYKCEECGKAFNRSSNLTK--HNIHTGEKSYKC--EECGKAFNQSSTLTKHRK 501
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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PROSITE; PS00028; ZINC_FINGER_C2H2_1; 12.
PROSITE; PS00157; ZINC_FINGER_C2H2_2; 14.
Hypotherical protein; Metal-binding; Nuclear protein; Zinc; Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1
644 AA; 74012 MW; A3CBF2437279B863 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (Fragment).
DKF2D5470168.
Homo sapiens (Human).
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Best Local Similarity
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256 IPDDLLKETEVKKLENLLDQGSKLNNLHELET-EKL-KVEEDEEDSEDSLD---EKRSDV 310
                                                                                     515 KP---YKCEECGKAFN---QSSNLTKHKIIHTGEKLYKCEECGKAFNRSSNLTTHKRIHT 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            393 KPYKCEECDKAFNRFSYLTKHKI-IHSGEKSYKCEQ--CGKGFNWSSTLTKHRIHTGEK 449
460 PYKCEECGKAFNVSSHLTTHKMIH---TGEKPYKCEEC--GKAFNHSSKL/TIHKIIHTGE 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          279 RENSYQC--EECDKVFKRFSTLTRHKRVHTGEKPFKC--EECGKAFKHSSTLTTHKMIHT 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81 EKKPFHCSVCGKGVNSRQHLKRHEITHT--KSFKCTFENÇQEAFYKHQSL-RHHILSVHE 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33S GEKPYRCEECGKAFYHSSHLTHKVIHTGEKPFKC--EECGKAFNHFSALTTHKFIHVKE 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          450 PYKCEBCGKAFNVSSHLTTHKMIH---TGEKPYKCEBC--GKAFNHSSKLTIHKIHTGE 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          256 IPDDLLKETEVKKLENLLDQGSKLNNLHELET-EKL-KVERDEEDEEDSLD---EKRSDV 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          138 KTLTCKQCNKVFTRPSKLAQHKLKHHGGSPAYQCDHPGCFKNFQTWSVLQFH--1KQSHP 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  196 KLKCPKCGKGCVGKKGLSSHMLSHDDSTMIKIWTCDYCDVGKFAKKNELVEHYNIFHDGN 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      505 KP---YKCEECGKAFN---QSSULTKHKIIHTGEKLYKCEECGKAFNRSSULTTHKRIHT 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 RPKKYICTYEGCDKAYNRPSLLEQHLRTHSNDRPYKCTVDDCDKAFFRKSHLETHIVSHS 80
                                                                                                                               311 RSDSMSAQRSIKSFTASLEGSKSVSKLISNSGKKINCPKNNCDRMFSREYDLRRHLK 367
                                                                                                                                                              569 GEKPYKCEECGKAFNRSSNLTK--HNIHTGEKSYKC--BECGKAFNQSSTLTKHRK 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tissues resting,

Tissues resting,

Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.

Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.

B GO: GO: 0005622; C: intracellular; IEA.

GO: GO: 0003676; F: nucleic acid binding; IEA.

GO: GO: 0005625; F: regulation of transcription, DNA-dependent; IEA.

R GO: GO: 0000555; F: regulation of transcription, DNA-dependent; IEA.

InterPro; IPR007087; Znf C2H2.

R InterPro; IPR007087; Znf C2H2.

R Frints: PR007087; Znf C2H2.

R PROSTIS; PR000064; Znr C2H2; 13.

R PROSTIS; PR000064; Znr C2H2; 11.

R PROSTIE; PS50005; KRAB; 1.

R PROSTIE; PS50005; KRAB; 1.

R PROSTIE; PS50005; KRAB; 1.

R PROSTIE; PS50015; Znr CFINGER C2H2 1; 12.

R PROSTIE; PS50015; Znr CFINGER C2H2 2; 14.

NON TER.

1 1 THON TER.

1 SEQUENCE 665 AA; 76467 MW; IABDALE4E00249DF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  311 RSDSMSAQRSIKSFTASLEGSKSVSKLISNSGKKINCPKNNCDRMFSREYDLRRHLK 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17.6%; Score 392; DB 4; Length 665;
32.5%; Pred. No. 3.7e-18;
iive 45; Mismatches 162; Indels 34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryofa, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                            Q86W65;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to zinc finger protein 91 (HPF7, HTF10) (Fragment).
                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 116; Conservative
                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Testis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                           QBGW65
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19;
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NINDMIYA K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H.,

RA Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara K.,

RA Greuta N., Sato K., Tanikawa E., Omura Y., Abe K., Kamihara K.,

RA Greuti T., Sato H., Wakameteu A., Ishii S., Yamamoto J., Isono Y.,

RA Aswai-Hio Y., Sato K., Nishikawa T., Kimura K., Yamashita H.,

RA Sariki Y., Sato K., Nishikawa T., Kimura K., Yamashita H.,

RA Kanehori K., Takahashi-Fujii A., Oshima A., Suyiyama A., Kawakami B.,

RA Kanehori K., Nakamura T., Sekine M., Kikuti H.,

RA Kanehori K., Nakamura T., Sekine M., Kikuti H.,

RA Kanehori K., Nakamura T., Sekine M., Kikuti H.,

RA Kanehori K., Nagahari K., Masuho Y., Nagai K., Isogai T.;

RE "NED, Popologia S., Pencalloperide activity, IEA.

BY OCCOMBA SEQUENCIAN NUCLEAR (BY SIMILARITY).

RENEL, AKOSELUTA ROCATRON: NUCLEAR (BY SIMILARITY).

RENEL, AKOSELUTA P. Funcalloperidase activity; IEA.

BY GO, GO.000327; F. Fincilo fon binding; IEA.

GO, GO.000327; F. Fincilo fon binding; IEA.

GO, GO.000528; P. Precallation of transcription, DNA-dependent; IEA.

BY GO, GO.000558; P. Pety M. S. BS.

BY GO, GO.000558; P. RAB.

BY REAM: PRO1322; KRAB.

REAM: PRO1322; KRAB.

REAM: PRO1322; KRAB.

REAM: PRO1322; RRAB.

REAM: PRO1322; RRAB.

REAM: PRO1322; RRAB.

REAM: PRO1322; RRAB.

REAM: PRO1322; RRAB.

REAM: PRO1312; PSO0142; ZINC_FINGER_CAR2; 16.

REPORTE: PSO0157; ZINC_FINGER_CAR2; 16.

REPORTE: PSO0142; ZINC_FINGER_CAR2; 16.

REPORTE: PSO0142; ZINC_FINGER_CAR2; 16.

REPORTE: PSO0142; ZINC_FINGER_CAR2; 16.

REPORTE: PSO0142; ZINC_FINGER_CAR2; 16.

REPORTE: PSO0142; ZINC_FINGER_CAR2; 16.

REPORTE: PSO0142; ZINC_FINGER_CAR2; 16.

REPORTE: PSO0142; ZINC_FINGER_CAR2; 16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KPFHCSVCGKGVNSRQHLKRHEITHT--KSFKCTFENCQEAFYKHQSLRHH----- 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  313 YVCERCGKAPKYSRILTTHKRIHTEEKPYKCNKCGKAFIASŠTLSRHEFIHM-GKKHYKC 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DHPGCFKNFQTWSVLQFH -- IKQSHPKLKCPKCGKGCVGKKGLSSHMLSHDDSTMIKIWT 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  372 EE--CGKAFIMSSVLTRHKRVHTGEKPYKCEECGKAFVASSTLSKHEIH+--TGKKPYK 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----ILSVH-----EKTLTCKQCNKVFTRPSKLAQHKLKHHGGSPAYQC 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 KKYICTYEGCDKAYNRPSILEQHIRTHSNDRPYKCTVDDCDKAFFRKSHLETHIVSHSEK 82
                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17.5%; Score 391; DB 4; Length 592; 31.1%; Pred. No. 3.8e-18; cive 41; Mismatches 161; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    592 AA; 67920 MW; D116FB9366EB4BDE CRC64;
                                                                           01-007-2002 (TrEMBLrel. 22, Created)
01-007-2002 (TrEMBLrel. 22, Last sequence update)
01-007-2003 (TrEMBLrel. 25, Last annotation update)
                                           592 AA
                                                                                                                                              Hypothetical protein FLJ39023.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 31.19
Matches 120; Conservative
                                           PRELIMINARY;
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zinc-finger.
SEQUENCE 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83
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                                       Q8N8Q4
Q8N8Q4;
RESULT 8
Q8N8Q4
                                           d
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288 - EKLKVEEDEEDEEDS----LDEKRSDVRSDSMSAQRSIKSFTASLEGSKSVSKLISNSGK 343
                                                           478 EKPYKCEECGKAFNOSSTLIKHKKIHTREKPYKCEECGKAF--HLSTHLTTHKILHTGEK 535
   230 CDYCDVGK-FAKKNELVEHYNIFHDGNIPDDLLKETEVKKLENLLDQGSKLNNLHELET- 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83 KPFHCSVCGKGVNSRQHLXRHBITHTKSFKCTFENCQBAFYKHQSL-RHHILSVHEKTLT 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              142 CKQCNKVFTRPSKLAQHKLKHHGGSPAYQCDHPGCFKNFQTWSVLQFH--IKQSHPKLKC 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       254 KPYKCEECGKAFNQFSNLTTHKKIHTGEQPYICEECGKAFTQSSTLTTHKRIHTGEKPYK 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23 KKYICTYEGCDKAYNRPSLLEQHLRTHSNDRPYKCTVDDCDKAFFRKSHLETHIVSHSEK 82
                                                                                                                                                                                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17.5%; Score 330; DB 4; Length 540; 30.0%; Pred. No. 4e-18; ive 61; Mismatches 155; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                540 AA; 62985 MW; 84D7D2EC15A7002C CRC64;
                                                                                                                                                                          01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
11-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypotheital protein FLJ36350.
Homo sapiens (Human).
                                                                                                                                                         540 AA.
                                                                                 344 KINCPKNNCDRMFSREYDLRRHLKWH 369
                                                                                                      536 PYRC - RECGKAFNHSATLSSHKKIH 559
                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 30.0%
Matches 107; Conservative
                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                 TISSUE=Thymus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zinc-finger
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                       Q8N211
                                                                                                                                     RESULT 9
                                                                                                                                               Q8N211
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559 GEKPYKCEECGKAFNRSSNLTK--HNIIHTGEKSYKC--BECGKAFNQSSTLTKHRK 611
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Ninonlya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H., Minonlya K., Wagatsuma M., Kikkawa E., Comray Y., Abe K., Kamihara K., Ratsuta N., Sato K., Tarikawa M., Yamazaki M., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamanica T., Irie R., Awai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamanita H., Isono Y., Amarina Y., Nakamura Y., Sekine M., Kikuchi H., Murakawa K., Yanachori K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K., Yanachori K., Takahashi-Fujii A., Oehima A., Sugiyama A., Kawakami B., Kanehori K., Takahashi-Fujii A., Oehima A., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Magalari K., Masuho Y., Nagai K., Isogai T., Ubmitted (OCT-2001) to the EMEL/GenBank/DDBJ databases.

1. Submitted (OCT-2001) to the EMEL/GenBank/DDBJ databases.

2. Submitted (OCT-2001) to the EMEL/GenBank/DDBJ databases.

3. Sin InterPro. IPRO07089; ZEC CZHZ.

3. RinterPro. IPRO07089; ZEC CZHZ.

3. RinterPro. IPRO07089; ZEC CZHZ.

3. RinterPro. IPRO07089; ZEC CZHZ.

3. RinterPro. IPRO07089; ZEC CZHZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         217 ECDKAFNOSSTLTTHKIIHTREKLNEYKECGKAFNQSSHLTRHKIIHTGEKPYKC--EEC 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      275 GKAFNQSSHLTRHKIIHTGEKPYKCEECGKAFRQSSHLTTHKIIHTGEKPYKC--EECGK 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 DKAFFRKSHLETHIVSHSEKKPFHCSVCGKGVNSRQHLKRHEITHT--KSFKCTFENCQE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 AFYKHQSL-RHHILSVHEKTLTCKQCNKVFTRPSKLAQHKLKHHGGSPAYQCDHPGCFKN 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        333 AFNKSSHLTRHKSIHTGEKPYQČEKCGKASNQSSNLTEHKNIHTEEKP-YKČEE--ČGKA 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               390 FNQFSNLTTHKRIHTGEKPYKCEECGKAFNQSSILTTHKRIH---TGEKSYKCEEC-GK 444
314 CEECGKAFNRSSKLTEHKNIHTGEQP-YKCEE--CGKAFNRSSNLTEHRKIHTEEKPYKC 370
                                                                            200 PKCGKGCVGXKGLSSHMLSHDDSTMIKIWTCDYCDVGK-FAKKNELVEHYNIFHDGNIPD 258
                                                                                                                                                    371 KECGKAFKHSSALTTHKRIH---TGEKPYKCEEC--GKAFNRSSKLTEHKKL-HTGK--- 421
                                                                                                                                                                                                                                              259 DLLKETEVKKLENLLDQGSKLNNLHELETEKLKVEEDE-----EDEEDSLDEKRSDVRSD 313
                                                                                                                                                                                                                                                                                                                          422 ----KPYKCEECGKAFIQSSKLTEHKKIHSGEIPYKCEECGKAFKHSSSLTTHKRIHTGEK 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62
                                                                                                                                                                                                                                                                                                                                                                                                                314 SMSAQRSIKSFTASLEGSKSVSKLISNSGKK-INCPKNNCDRMFSREYDLRRHLKWH 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 479 PYKCEECGKAFSRS---SKLTEHKIIHTGEKPYKCER--CDKAFNQSANLTKHKKIH 530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 ESDETKSISSLISSSSSSRPKKYICTYEGCDKAYNRPSLLEQHLRTHSNDRPYKCTVDDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryotta, Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini, Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72;
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Prodom, PD000003; Znf C2H2; 2.
PRODOMSS5; Znf CZH2; 2.
PROSITE; PS00025; Znc Zh2; 1; 10.
PROSITE; PS00157; ZINC FINGER C2H2 1; 10.
PROSITE; PS0157; ZINC FINGER C2H2 2; 16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17.5%; Score 390; DB 4; Length 576; 28.6%; Pred. No. 4.3e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28.6%; Pred. No. 4.3e-10,
tive 57; Mismatches 168; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     576 AA; 66620 MW; 4396672D34BF99CD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein FLJ31526.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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SEQUENCE 5
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Matches
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RA Adams M.D. (Sciniker S.E., 110 P.W., Bryans C.A., Gocayne J.D., RA Adams M.D. (Sciniker S.E., 110 P.W., Bryans C.A., Gocayne J.D., RA Adams M.D., Scherer S.E., 11 P.W., Bryans C.A., Chan L.X., George R.A., Lewis S.E., Richards S., Ashburner M. L.X., Randerson S.N., Raderson S.N., Randell M.D., Zhang Q., Chan L.X., R. Bruton G.G., Worthan J.R., An H.-Q., Adherson C.R., Mikhos G.L.G., Randon R.C., Ragars Y. H.C., Blazej R.G., Change M., Mikhos G.L.G., Raldwin D., Rall J.F., Addrews Pfemankoch C., Baldwin D., Rall Salles R.A., Barchaale J., Bayzakarsoglu L., Beasley E.M., Balle R.W., Beuck J., Sectoral M.R., Bouck J., Endrews Pfemankoch C., Baldwin D., Ra Burtis R.C., Busam D.A., Buller H., Cadieu E., Cener A., Chandra I., Rockova D., Botcham M.R., Bouck J., Burder B., Cener A., Chandra I., Rockova D., Botcham D.A., Buller H., Cadieu E., Cener A., Chandra I., Raburtis R., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Cadieu E., Caner J.W., Cawley S., Dahlke C., Davangort L.B., Davies P., Rapen C.C., Rays A.D., Dew I., Dietz S.M., Dodoon K., Orong E., Gorrell J.H., Gu Z., Gdan P., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Lin X., Mattel B., Morintosh T.G., Wei M.-H., Ibegwam C., Alalli M., Kalush F., Karpen G.H., M., Meiner D., Marker D., Lin X., Mattel B., Morintosh T.C., Morris J., Morris D., Lin X., Mattel B., Morintosh T.C., Morris J., Morris M., Nalsen D.L., Rainer K., Remington K., Petulos M., Murphy L., Murzhy D.M., Nalsen D.L., Shen H., Shier E., Spradling A.C., Stapleton M., Stupski M.P., Shu H., Wang X., Hang X., Shier H., Shong F.N., Weinsenbach J., Wang X., Shier H., Zhong F.N., Weinsenbach J., Wang X., Shier Y., Lander S., Wang X., Land X., Marte B., Sharing F.N., Weinsenbach J., Wang X., Shier H., Shong F.N., Rondon F.N., Weinsenbach J., Wang X., Shier H., Shong F.N., Rondon F.N., Weinsenbach J., Shier S., Shier S., Shier S., Shier S., Shier S., Shier S., Shier S., Shier S., Shier S., Shier S., Shier S., Shier S., Shier S.
238 -FAKKNELVEHYNIFHDGNIPDDLLKETEVKKLENLLDQGSKLNNLHELETEKLKVEEDE 296
                                        445 AFYRSSKLITEHKKI-HIGEKP------YTCEECGKAFNHSSHLAIHKV-IHTGE
                                                                                        297 EDEEDSLDEKRSDVRSDSMSAQRSIKSFTASLEGSKSVSKLISNSGKKINCPKNNCDRMF
                                                                                                                                     491 KPYQ-------CEECGKAFNQSSHLTR--HKRIHTGEKPYQCEK--CGKAF
                                                                                                                                                                                   357 SREYDLRRHLKWHDDNLQRIESFLNSIEKEETPEGEPLVKKARMDLLPNETSVISR 412
                                                                                                                                                                                                                              531 NOSSNITGHKKIH-------TGEKLYKPKRCNSDFENTSKFSK 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoplera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last segu
01-JUN-2003 (TrEMBLrel. 24, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly)
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HSSP; P08047; 1SP2.
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                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CG5245 protein.
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Q9VG72
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SMART; SM00349; KRAB; 1
                                                                                                                                                       Query Match
Best Local Similarity
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Q80VH2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-----DDLLKETEVKKLENLLDQ-GSKLNNLHELETE----KLKVEEDEEDSL 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           304 DEKRSDVRSDSMSAQRSIKSFTASLEGSKSVSKLISNSGK-KINCPKNNCDRMFSRBYDL 362
                                                                                                                                                                                                                                                        80
                                                                                                                                                                                                                                                                                                                                                                                                                                  21 RPKKYICTYEGCDKAYNRPSLLEQHLRTHSNDRPYKCTVDDCDKAFFRKSHLETHIVSHS
                                                                                                                                                                                                                                                                          81 EKKPFHCSVCGKGVNSRQHLKRHEITH--TKSFKCTFENCQEAFYKHQSLRHHILSVHEK
                                                                                                                                                                                                                                                                                                                                                      TLTCKQCNKVFTRPSKLAQHKLKHHGGSPAYQCDHPGCFKNFQTWSVLQFHIKQSHPK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LKCPKCGKGCVGKKGLSSHMLSHDDSTMIKIWTCDYCDVGKFAKKNELVEHYNIFHDGNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          359 PFKCTHCFKDFKCRTHLR--VHMLDHIGEKVPKCSYCSKEFKLSSQLLVHLQEHTGKNQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
TRARE-binding zinc finger protein.
TRARE-binding zinc finger protein.
Enkaryota Spiens (Human).
Eukaryota Katavoa (Dordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                 53;
                                                                                                                                                                          Length 501;
                                                                                                                                                                      17.4%; Score 388.5; DB 5; Length 29.7%; Pred. No. 4.6e-18; tive 63; Mismatches 142; Indels
                                                                                                                                     BBAE04740D41C43F CRC64;
                    Pfam; PF00096; zf-C2H2; Ī5.
ProDom; PP000003; znf_C2H2; 3.
SMAKT, SM0355; ZnF_C2H2; 3.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; 14.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 15.
Metal-binding; Zinc; ZInc_finger.
SEQUENCE 501 AA; S8790 WW; BBAE04740D
InterPro, IPR007087; Znf_C2H2
                                                                                                                                                                            Query Match
Best Local Similarity 29.7%
Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          303 LDEKRSDVRSDSMSAQRSIKSFTASLEGSKSVSKLISNSGKK-INCPKNNCDRMFSREYD 361
                                                                                                                                                                                                                                                                                                                                        70
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STAIN—FUP/N; TISSUE—Breast tumor;
STAIN—FUP/N; TISSUE—Breast tumor;
STAIN—FUP/N; TISSUE—Breast tumor;
STAIN—FUP/N; TISSUE—Breast tumor;
STAIN—FUP/N; TISSUE—Breast tumor;
SUDMILLEG (MAR-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; BCG49144; AAH9144.1; -.
GO; GO:0005622; C:intracellular; IEA.
GO; GO:0005632; C:intracellular; IEA.
GO; GO:0006335; P:regulation of transcription, DNA-dependent; IEA.
R GO; GO:000635; Erregulation of transcription, DNA-dependent; IEA.
R InterPro; IPRO01909; XRAB;
R InterPro; IPRO01909; XRAB; 1.
PFam; PF001352; KRAB; 1.
PRAMT; SM00354; KRAB; 1.
R SMART; SM00355; ZIF C2H2; 15.
R PROSITE; PS00028; ZINC C2H2, 15.
R PROSITE; PS00028; ZINC FINGER_C2H2_2; 15.
R PROSITE; PS00028; ZINC FINGER_C2H2_2; 15.
R PROSITE; PS00028; ZINC FINGER_C2H2_2; 15.
R PROSITE; PS00028; ZINC FINGER_C2H2_2; 15.
R PROSITE; PS00028; ZINC FINGER_C2H2_2; 15.
                                                                                                                                                                                                                                                                                                                                                                            71 HLETHIVSHSEKKPFHCSVCGKGVNSRQHLKRHEITHTKSFKCTFENCOEAFYKHQSL-R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              130 HHILSVHEKTLTCKQCNKVFTRPSKLAQHKLKHHGGSPAYQCDHPGCFKNFQTWSVLQFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           330 HKRIHTGEKPYKCEECGKAFNRSSKLTEHKNIHTGEQP-YKCEE--CGKAFNRSSNLTEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        248 YNIFHDGNIPDDLLKETEVKKLENLLDQGSKLNNLHELETEKLKVEEDE-----EDEEDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    442 YKKLHTGK------KPYKCBECGKAFIQSSKLTEHKKIHSGEIPYKCEECGKAFKHSSSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 SSSSSSPPKKYIC----TYEGCDKAYNRPSLLEQHLRTHSNDRPYKCTVDDCDKAFFRKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                     Length 568
PROSITE; PS50805; ARAB; 13.
PROSITE; PS50805; KRAB; 1.
PROSITE; PS508028; ZINC FINGER C2H2 1; 9.
PROSITE; PS5017; ZINC FINGER C2H2 2; 14.
Metal-bining; Zinc; Zinc-finger.
SEQUENCE 568 AA; 66222 MW; 3BBC819822B89940 CRC64;
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Last annotation update)
                                                                                                                                                                                                                  17.4%; Score 388; DB 4; L. 28.5%; Pred. No. 5.7e-18; ative 62; Mismatches 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similar to zinc finger protein 97.
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01-JUN-2003 (TrEMBLrel. 24,
01-JUN-2003 (TrEMBLrel. 25,
01-OCT-2003 (TREMBLREL. 25,
                                                                                                                                                                                                                                                                               Matches 105, Conservative
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Search completed: May
Job time : 46 secs
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Matches
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                        17;
                                                                          242
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                                                                                                                            243 KPYKCNQCDKAFSQYSHLHIHRRTHİGEKPLKCNECDEİFSNHSNLQTHRRIHIGEKPYK 302
                                                                                                                                                     ---CQEAFYKHQSLRHHILS-VHEKTLTCKQCNKVFTRPSKLAQHKLKHHGGSPAYQCDH 173
                                                                                                                                                                       303 CNQCDKARSQHSTLQNHRRTHTGEKPFKCNQCDKAFSRHSTLQTHRRTHTGEKP-FKCNQ 361
                                                                                                                                                                                                          174 PGCFKNFQTWSVLOFHIKQSH---PKLKCPKCGKGCVGKKGLSSHMLSHDDSTMIKIWTC 230
                                                                                                                                                                                                                         --CDKAFSQYSHLHIH-RRIHTGEKPFKCNQCNKAFSQYSHLHIHRRTH---TGEKPYKC 415
                                                                                                                                                                                                                                                          DYCDVGKFAKKNELVEHYNIFHDGNIPDDLLKETEVKKLENLLDQGSKLNNLHELETEKL 290
                                                                                                                                                                                                                                                                                    NQCD--KIFSNHSTLQTHRRTHTGE-----KPYKCNQCDKAFSRHSTLQTHRRTHTGEK 467
                                                                                                                                                                                                                                                                                                             291 KVEEDEEDEEDELDEKRSDVRSDSMSAQRSIKSFTASLEGSKSVSKLISNSGKKI-NCPK 349
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MEDLINE=22354683; PubMed=12466851;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I will Team;
Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:553-573 (2002).
EMBL; AK032220; BAC27766.1; -
InterPro; IPR007087; Znf C2H2.
InterPro; IPR007086; Znf C2H2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23 KKYICTYEGCDKAYNRPSILEQHIRTHSNDRPYKCTVDDCDKAFFRKSHLETHIVSHSEK
                                                   23 KKYICTYEGCDKAYNRPSLLEQHLRTHSNDRPYKCTVDDCDKAFFRKSHLETHIVSHSEK
                                                                   Gaps
                          Gaps
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01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
MSZF33 homolog
Mus musculus (Mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
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                          80;
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Length 559;
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17.4%; Score 387; DB 11; Length 5:
28.7%; Pred. No. 6.6e-18;
.ive 55; Mismatches 136; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Prem; Pro0056; zf-C2H2; 8.

PRINTS; PR00048; ZINCFINGER.
SMART; SM00355; ZnF C2H2; 8.

PROSITE; PS00029; ZINC FINGER C2H2 1; 8.

PROSITE; PS50127; ZINC FINGER C2H2 2; 8.

SEQUENCE 297 AA; 34666 MW; 2B94CC27CB2635EB CRC64;
                                                                                                      KPFHCSVCGKGVNSRQHLKRHEITHT--KSFKC----TFEN--
                                                                                                                                                                                                                                                                                                                                         468 PFKCNQCDK------AFSOKCSLOKHIRIHT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                            297
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                                                                                                                                                                                                                                                                                                                                                                                    NECDKAFSOHSTLOTHRRTH 519
Query Match
Best Local Similarity 28.7<sup>3</sup>
Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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Matches 9
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194 VHTGEKPYKCSECDKGFTSKSRLNIHQRVHTGEKSYKCS--ECDKSFSQQGNLSIH-LRI 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           308 MGEKPYKCSECDKGFTQKCRLIHQIHHTGKKGYKCSECDKC----FILKSDLSIHQRI- 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      138 TNNREKTYKCS--ECDKCFTKKCKLRQHQRIHTGEKPYKCS--ECDKCFTQKDRLIHQR 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      H--EKILICKOCNKVFTRPSKLAQHKLKHHGGSPAYQCDHPGCFKNFQTWSVLQFH--IK 191
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                                                                                                                                                                          195 PKLK---CPKCGKGCVGKKGLSSHMLSHDDSTMIKIWTCDYCDVGK-FAKKNELVEHYNI 250
                                                                                                                                                                                                       234 TGEKEYECEĞCGKAFANQSYFQVHKRIH---TGEKPYKCDQC--GKAFVGSSDLKRHERV 288
194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SHSEKKPFHCSVCGKGVNSRQHLKRHEITHT - - KSFKCTFENCQEAFYKHQSLRHHILSV
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                                                                               T-----CKQCNKVFTRPSKLAQHKLKHHGGSPAYQCDHPGCFKNFQTWSVLQFHIKQSH
                                                                                                                             TGEKPYKCNECGKAPARHSHLKVHKITHTGEKP-YKCNQ--CGKALAYHSTLQVH-QRTH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -SYKCSECDKSFTQ--QGNLRIHLRIHTGEKPYKC--SECDKCFTYKSGLRSH 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 511;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases. Submitted (DEC-2001); AAH19219.1; -.
InterPro; IPR007087; Znf C2H2.
InterPro; IPR007087; Znf C2H2.
IPfam; PR00015; Znr C2H2; 12.
PROSITE; PS00028; Znr C2H2; 12.
PROSITE; PS01057; Znr FINGER C2H2_1; 12.
Metal-binding; Zinc; Zinc* finger.
SEQUENCE 511 AA; 59582 MW; 11C75B5B38F2DB6F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OL-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-WAR-2003 (TrEMBLrel. 24, Last annotation update)
Similar to zinc finger protein 40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match 17.1%; Score 382; DB 11; Local Similarity 31.1%; Pred. No. 1.3e-17; les 110; Conservative 47; Mismatches 143:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               511
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Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

May 5, 2004, 15;15:26 ; Search time 17 Seconds (without alignments) 1261.936 Million cell updates/sec

US-09-831-804-3 2229 1 MSESDETKSISSLISSSSSS.....PLVKKARMDLLPNETSVISR 412 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 segs, 52070155 residues

Searched:

Total number of hits satisfying chosen parameters:

141681

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ΩI	A YEAS		ZN43 HUMAN	Z492_HUMAN	TF3A HUMAN	ZN85 HUMAN	ZN93 HUMAN	ZN91 HUMAN	Z347 HUMAN	Z431 HUMAN	Z228 HUMAN	30	Z184 HUMAN	XFIN XENLA	Z257_HUMAN	Z436_HUMAN	ZN84 HUMAN	ZN41 HUMAN	ZF46 MOUSE	KR18 HUMAN	ZN83 HUMAN	ZO71_XENLA	ZZZ6_HUMAN	PRD5_HUMAN	Z429 HUMAN	Z208 HUMAN	YD49_HUMAN	Z155 HUMAN	Z271 HUMAN	Z234 HUMAN	Z305 HUMAN	Z141_HUMAN	12
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P17020 homo sapien Q9uk10 homo sapien	O9ngz8 homo sapien P18747 xenopus lae	Q9ul59 homo sapien Pl6374 mus musculu	Q9ukl3 homo sapien 014709 homo sapien 09uid9 homo sapien	234695 rana pipien P17027 homo sapien
ZN16_HUMAN Z225_HUMAN	ZN71 HUMAN ZO28 XENLA ZN2E LITMAN	Z214_HUMAN ZF60_MOUSE	Z221_HUMAN Z197_HUMAN Z255_HUMAN	TF3A_RANPI ZN23_HUMAN
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670	4 4 4 8 8 8 9 9 9	606	617 1029 623	335 643
15.7	15.7	15.6	15.6 15.6 15.6	15.5
350	348.5	348	348 347 46	345.5
3.5 3.5	33.0	9.64	4 4 4 4 2 2 4	4 4 5

ALIGNMENTS

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         TF3A_SCHPO
                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the butopean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    236 GKFAKKNELVEHYNIFH-DGNIPDDL-LKETEVKKLENLLDQGSKLNNLHELETEKLKVF 293
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                                                                                                                                                                                                                                       SGD; S0006390; PZFI.

GO; GO:0005667; C:transcription factor complex; IPI.

GO; GO:0005709; F:RNA polymerase III transcription factor act. . ; IPI
GO; GO:0005384; P:RNA polymerase III transcription III promoter; IPI.

InterPro; IPR007087; Zf C2H2.

FFam; PF00096; Zf C2H2.

SWART; SM00355; Zn C2H2.

PROSITE; PSF00128; ZINC FINGER C2H2.1; 8.

PROSITE; PSF00129; ZINC FINGER C2H2.2; 6.

Transcription regulation; Zinc Finger; Metal-binding; DNA-binding;

FNA-binding; Repeat; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83 -- DKCAKSFVKKSHLERHLYTHSDTKPPQCSYCGKGVTTRQQLKRHEVTHTKSFICPEEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          261 MSFSRKHDLLTHYGSIHTEEDIPLELKYKISDIQQL--VQDHGVQLGN----SKHSNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58 TVDDCDKAFFRKSHLETHIVSHSEKKPFHCSVCGKGVNSRQHLKRHEITHTKSFKCTFEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CQEAFYKHQSLRHHILSVHEKTLTCKQCNKVFTRPSKLAQHKLKHHGG--SPAYQCDHPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          141 CNLRFYKHPOLRAHILSVHLHKLTCPHCNKSFORPYRLRNHISKHHDPEVENPYÖCTFAG
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209B1EDEA20422D9 CRC64;
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                                                                                                                                                              EMBL; M90638; -; NOT_ANNOTATED_CDS.
EMBL; U25841; AAB64615.1; -.
PIR; $20060; $20050.
Germonline; 144451; -.
TRANSFAC; T03530; -.
SUBCELLULAR LOCATION: Nuclear
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Matches 174; Conservative
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10. TFTA, SCHENO STRUDARD, RRT, 374 AA.

OSTITIA, CONTROL (AL.) ALL CEMENDARD, RRT, 374 AA.

DE TERE-2003 (Red.) 41, CEMENDARD, RRT, 374 AB.

OR STRUCK (RED.CLAIL CONTROL AND ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED ARRENDED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 HISACHTHLLPYPCTYODCELRFATKOKLONHVNRAHEKIISYSCPHESCVGHEGFEKWS 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  185 VLOFHIKQSHPKLKCPKCGKGCVGKKGLSSHMLSHDDSTMIKIWTCDYCDV----GKFAK 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EDBEDSLDEKRSDVRSDSMS--AQRSIKSFTASLEGSKSVSKLISNSGKKINCPKNNCDR 354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  193 QLQNHIREAHVP-SCSICGRQFKTAAHLRHYVVLH--QTTLEERKTYHCPMEGCKKSFTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 SSSSSSRPKKYICTYEGCDKAYNRPSILEQHLRTHSNDRPYKCTVDDCDKAFFRKSHLET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 KNELVEHYNIFHDGNIP---DDLLKETEVK-KLENLLDQGSKLNNLHELETEKLKVEEDE
PROSITE, PS00028, ZINC_FINGER_C2H2_1, 8.
PROSITE; PS50157, ZINC_FINGER_C2H2_2, 9.
Transcription_regulation; Zinc-finger; Metal-binding; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Lovering R., Trowsdale J.,
"A gene ancoding 22 highly related zinc fingers is expressed in
lymphoid cell lines." 19:2921-2927 (1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZN43 HUMAN STANDARD; PRT; 803 AA.
P17058, P2816.0, Q96D61,
01.AUG-1990 (Rel. 15, Created)
01.DEC-1992 (Rel. 24, Last sequence update)
10.OCT-2003 (Rel. 42, Last annotation update)
Zinc finger protein 43 (Zinc protein HTF6) (Zinc finger protein KOX27).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34;
                                                                                                                                                                                                                                                                                                                                                                                                                  22.2%; Score 495; DB 1; Length 374; 32.8%; Pred. No. 1.6e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58; Mismatches 160; Indels
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W; 7469C701FFF08FF CRC64;
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                                                                on requiactou, .....; Repeat; Nuclear D 23 47 C 53 77 C 6 83 107 C 113 138 C 144 169 C 236 226 C 236 226 C 236 291 349 374 AA; 43851 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                       RNA-binding;
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Matches 123;
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ID ZN43 H
DD ZN43 H
DD IO -AUG
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DB ZOCK
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MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopking R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Altschul S.F., Zeeberg B., Berdew K.H., Studin G.M., Hong L.,
Batchenko L., Marusha K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Brownstein M.J., McMennan K.J., Malek J.A., Glubs R.D.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Glubs R.B.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,
Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Glibs R.A.,
Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakeeley R.W., Touchman J. W., Green B.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Chenrick A., Schein J.E., Jones S.J.M., Marra M.A.,
"Generation and initial analysis of more than 15,000 full-length
Inman and mouse cDNA sequences.",
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Martial J.A.;
"The evolutionarily conserved Kruppel-associated box domain defines a subfamily of eukaryotic multifingered proteins.";
Proc. Natl. Acad. Sci. U.S.A. 88:3608-3612(1991).
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-!- SUBCELLULAR LOCATION: Nuclear (Probable).
-!- TISSUE SPECIFICITY: T AND B CELL LINES.
-!- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-FINGER PROTEINS.
-!- SIMILARITY: Contains 1 KRAB domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [3]
SEQUENCE OF 38-190 FROM N.A.
MEDLINE=91219421; PubMed=2023909;
Bellefroid E.J., Poncelet D.A., Lecocg P.J., Revelant O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PSS0805; KRAB; 1.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; 19.
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MIM; 603972; ...

MIM; 603972; ...

MICON GO:1003677; F:DNA binding; TAS

GO: GO:1003677; F:DNA binding; TAS

INTERPRO; IPR001909; ZNF C2H2.

INTERPRO; IPR007086; ZNF C2H2.
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MEDLINE-91145339; PubMed=2288909;
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Pfam; PF00096; zf-C2H2; 21.
PRINTS; PR00048; ZINCFINGER.
Prodom; pD000003; ZIL C2H2; 16.
SMART; SM00349; KRAB; 1.
SMART; SM00355; ZNF C2H2; 22.
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EMBL; M61869; AAA58674.1; -.
EMBL; X52358; CAA36584.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 476-531 FROM N.A.
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New Biol. 2:363-374(1990)
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HSSP; P08048; 7ZNF.
TRANSFAC; T04986; -.
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Euteleostomi;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E-DEEDEEDSLDEKRSDVRSDS--MSAQRSIKSFTASLEGSKSVSKLISNSGKKINCPKN 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       367 IECGEAFSRSSNLTKHKKIHTEKKPYKC--EECGKAFKWSSKLTEHKLTHTGEKPYKC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EECGKAFNWPSTLIKHNRIHTGEKPYKCEVCGKAFNQFSNLTTHKRIHTAEKPYKC--EE
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PROSITE; PS50157; ZINC_FINGER_C2H2_2; 22.
Transcription regulation; DNA-binding; Zinc-finger; Metal-binding;
Nuclear protein; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17.9%; Score 400; DB 1; Length 803; 31.9%; Pred. No. 1.4e-16;
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                                                                                                                                                                                                                                                                           803 AA;
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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Zinc finger protein 492 (Fragment).
Homo sapiens (Human).

RESULT 4
2492 HUMAN
D 2492 BUMAN
AC 09P255;
DT 28-FEB-2003
DT 15-MAR-2004
DE Zinc finger
GN ZNR492 OR KI.

574 AA

PRT;

STANDARD;

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                                                                                                                                                                    Nagase T., Kikuno R., Ishikawa K.-I., Hirosawa M., Ohara O.; "Prediction of the coding sequences of unidentified human genes. XVII. The complete sequences of 100 new cDNA clones from brain which code
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PROSITE; PS50805; ZINC_FINGER_C2H2_1; 12.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 13.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 13.
Hypothetical protein; Transcription regulation; DNA-binding; Sinc-finger; Metal-binding; Nuclear protein; Repeat.
                                                                                                                                                                                                                                                       for large proteins in vitro.";

DNA Res. 7:143-150(2000).
-!- FUNCTION: May function as a transcription factor.
-!- SUBCELLULAR LOCATION: Nuclear (Probable).
-!- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE PINGER PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17.9%; Score 398; DB 1; Length 574; 30.2%; Pred. No. 1.3e-16; ive 48; Mismatches 167; Indels
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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C2H2-TYPE.
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InterPro; IPR001099; KRAB.
InterPro; IPR007087; Znf_CZH2.
InterPro; IPR007088; Znf_CZH2.eub.
Pfam; PF001352; KRAB; 1.
Pfam; PF00096; Zf-CZH2; 13.
PRINTS; PR000009; Znf_CZH2; 2.
SMART; SM00349; KRAB; I.
SMART; SM00355; Znf_CZH2; 13.
                                                                                                                              TISSUE=Brain;
MEDLINE=20277482; PubMed=10819331;
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Genew; HGNC:23707; ZNF492.
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                                                NCBI_TaxiD=9606;
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99; Conservative
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223
378
423 AA;
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(Rel.
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01-OCT-1996
10-OCT-2003
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ID ZN85 HUMAN
AC Q03923;
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255 NIPDDLLKETEVKKLENLLDQGSKLNNLHELETEKLKVEEDEEDEEDSLDEKRSDVRSDS 314
                                                                                                   433 EXP---YKOEBCGKAFNLSSQLTTHKIIHTGE-KPYKCEEC------GKAFNQSST 478
                                                                                                                                    361
                                      254
                                                                                                                                                        479 LSKHKVIHTGEKPYKYEECGKAFNOS--SHLTTHKMIHTGEKPYKC--EECGKAFNNSSI 534
                                      195 PKLKCPKCGKGCVGKKGLSSHMLSHDDSTMIKIWTCDYCDVGKFAKKNELVEHYNIFHDG
                                                                                                                                 315 MSAQRSI------KSFTASLEGSKSVSKLISNSGKKINCPKNNCDRMFSREYD
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=94342241; PubMed=8063702;
Moorefield B., Roeder R.G.;
"Purification and characterization of human transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

TISSUE-Fetal brain;

MEDLINE-95309028; PubMed=7789179;

Arakawa H., Nagase H., Hayashi N., Ogawa M., Nagata M.,

Fujiwara T., Takahashi E., Shin S., Nakamura Y.;

"Molecular cloning, characterization, and chromosomal mapping in ovel human gene (GTF3A) that is highly homologous to Xenopus transcription factor IIIA.";

Cytogenet. Cell Genet. 70:235-238(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUB=Brain;
MEDLINE=95347600; PubMed=7622052;
Drew P.D., Nagle J.W., Canning R.D., Ozato K., Biddison W.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Becker K.G.; "Cloning and expression analysis of a human cDNA homologous
                                                                                                                                                                                362 LRRHLKWHD-------DNLQRIESFLNSIEKEE 387
                                                                                                                                                                                                       LNRHKMIHTGEKLYKPESCNNACDNIAKISKYKRNCAGEK 574
                                                                                                                                                                                                                                                                  TF3A HUMAN STANDARD; PRT; 423 AA. Q92664; Q12963; Q13097; Created) 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Transcription factor IIIA (Factor A) (TFIIIA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OF OTHER GENES.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- TISSUE SPECIFICITY: Ubiquitous.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 61-423 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xenopus TFIIIA.";
Gene 159:215-218(1995).
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CHARACTERIZATION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        196
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BSVSSLTIADAFIAAGESSAPTPPRPALPRRFICSFPDCSANYSKAWKLDAHLCKHTGER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 KSISSL-----ISSSSSR----PKKYICTYEGCDKAYNRPSLLEQHLRTHSNDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        108 TKSFKCTFENCQEAFYKHQSLR-HHILSVHEKTLTCKQ--CNKVFTRPSKLAQHKLKHHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54 PYKCIVDDCDKAFFRKSHLEIHIVSHSEKKPFHCSV - CGKGVNSRQHLKRH-BITH---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C2H2-TYPE

C2H2-TYPE

C2H2-TYPE

C2H2-TYPE

CAH2-TYPE

CAH2-TYPE

V -> L (in dbSNP:7323).

/FTIG-PAR (014824).

N -> H (IN REF. 2). AAA21873).

MISSING (IN REF. 2; AAA21873).

SILASHLGGYI -> EFGLSSQWIY (IN REF. 1).

W; A627D064A43FB6FO CRC64;
                                                                                        REMEL; D32257; BAA06988.1; -.

REMEL; U20722; AAA7523.1; -.

REMEL; U14134; AAA21873.1; -.

REMEL; U14134; AAA21873.1; -.

REMEL; U14134; AAA21873.1; -.

REMEL; U14134; AAA21873.1; -.

REMER; P03001; IPF3.

REMER; P03001; IPF3.

REMER; P0009303; P:RNA polymerase III transcription factor act. ..;

RO; GO:0003303; P:RNA transcription; TAS.

RO; GO:0005303; P:RNA cription from Pol III promoter; TAS.

REMER; PRO0096; ZF-C2H2; 9.

REMER; PS00098; ZRC C2H2; 9.

REMER; PS00098; ZINC FINGER C2H2 1; 7.

REMER; PS0157; ZINC FINGER C2H2 1; 7.

REMER; PS0157; ZINC FINGER C2H2 1; 7.

REMER; PS0157; ZINC FINGER C2H2 1; 7.

REMER; PS0157; ZINC FINGER C2H2 1; 7.

REMER; PS016018; ZINC FINGER C2H2 1; 7.

REMER; PS016018; ZINC FINGER C2H2 1; 7.

REMER; PS016018; ZINC FINGER C2H2 1; 7.

REMER; PS016018; ZINC FINGER C2H2 1; 7.

REMER; PS016018; ZINC FINGER C2H2 1; 7.

REMER; PS016018; ZINC FINGER C2H2 1; 7.

REMER; PS016018; ZINC FINGER C2H2 1; 7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17.8%; Score 397.5; DB 1; Length 423; 31.1%; Pred. No. 9.9e-17; ive 55; Mismatches 95; Indels 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               165 GSPAYQCDHPGCFKNFQTWSVLQFHIKQSHPK-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE (ATYPICAL).
C2H2-TYPE.
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Last annotation update)
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                                                                                                                                                                                      MEDLINE-9905377; PubMed=9839802; MEDLINE-9905377; PubMed=9839802; Poncelet D.A., Ballefroid B.G., Bastiaens P.V., Demoitie M.A., Marine J.C., Pendeville H., Alami Y., Devos N., Lecocq P.J., Ogawa T., Muller M., Martial J.A.; Muller M., Martial J.A.; Prunctional analysis of ZNF95 KRAB zinc finger protein, a member of the highly homologous ZNF91 family."; DNA Cell Biol. 17:931-943(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- DEVELOPMENTAL STAGE: Expressed early during embryonic development.-!- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-FINGER PROTEINS.-!- SIMILARITY: Contains 1 KRAB domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE: PS50805; KRAB: 1.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; 14.
PROSITE; PS00028; ZINC_FINGER_C2H2_2; 15.
TRANSCTED; PS50187; ZINC_FINGER_C2H2_2; 15.
Transcription regulation; Zinc-finger; DNA-binding; Metal-binding;
Nuclear protein; Repeat; Repressor.
                                                               Craniata, Vertebrata, Euteleostomi,
Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MIM, 50.09393; Cinucleus, TAS.

GO; GO:0003714; Fitranscription co-repressor activity; TAS.

GO; GO:0003700; Fitranscription factor activity; TAS.

GO; GO:0003700; Fitranscription factor activity; TAS.

InterPro; IPR001087; Znf_C2H2.

InterPro; IPR007086; Znf_C2H2.

Ffam; PF01352; KF-C2H2, 15.

PRINTS; PR00048; ZINCFINGER.

ProDom; PD000003; Znf_C2H2; 13.

SMART; SM00349; KZAB; 1.

SMART; SM00355; Znf_C2H2; 13.
                                                                                                                                                                                                                                                                                                                                                       [2]
SEQUENCE OF 1-196 FROM N.A.
MEDLINE=91219421; PubMed=2023909;
Bellefroid B.J., Poncelet D.A., Lecocq P.J., Revelant O.
Martial J.A.;
    finger protein 85 (Zinc finger protein HPF4) (HTF1)
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C2H2-TYPE (DEGENERATE)
C2H2-TYPE.
                                                                                                                                                     SEQUENCE FROM N.A., AND CHARACTERIZATION.
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C2H2-TYPE.
C2H2-TYPE.
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EMBL; M61866; AAA52689.1; -.
EMBL; M61868; AAA58671.1; -.
PIR; C39384; C39384.
PIR; G02075; G02075.
HSSP; P08048; 7ZNR.
TRANSFAC; T04990; -.
Genew; HGNC:13160; ZNP85.
                                                               Bukaryota; Metazoa; Chordata;
Mammalia; Butheria; Primates;
NCBI_TaxID=9606;
                                                 Homo sapiens (Human)
                                                                                                                                                                               TISSUE=Placenta;
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ZN_FING
ZN_FING
ZN_FING
ZN_FING
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12 TLTKHKIIHTGE-----KPYKSKECEKAFNQSSKL-----TEHKKIHTGEKPYE--- 455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SL-RHHILSVHEKTLICKQCNKVFTRPSKLAQHKLKHHGGSPAYQCDHPGCFKNFQTWSV 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69 KSHLETHIVSHSEKKPFHCSVCGKGVNSRQHLKRHEITHT--KSFKCTFENCQEAFYKHQ 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   242 SSNLIKHKTHTGEKPYKCEECGKAFNRESTLTTHKIIHTGEKPYKC--KECGKAFNRSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            186 LQFH--IKQSHPKLKCPKCGKGCVGKKGLSSHMLSHDDSTMIKIWTCDYCDVGKFAKKNB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           244 LVEHYNIFHDGNIPDDLLKETEVKKLENLLDQGSKLNNLHELETEKLKVEEDEEDESL
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Lamerdin J.E., McCready P.M., Skowronski E., Sakaldasis G.,

Lamerdin J.E., McCready P.M., Dias J., Scott D., Stilwagen S.,

Burkhart-Schultz K., Gordon L., Dias J., Scott D., Stilwagen S.,

Phan H., Velasco N., Do L., Regala W., Terry A., Danganan L.,

Brier A., Christensen M., Georgescu A., Avila J., Attix C.,

Andreise T., Trankheim M., Amico-Keller G., Coefield J., Duarte S.,

Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B., Arellano A.,

Sanders C., Ow D., Nolan M., Trong S., Kobayashi A., Olsen A.S.,

Carrano A.V.;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
10.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZN93 HUMAN STANDARD; PRT; 616 AA.
P35789; Q9YZN8;
01-UUN-1994 (Rel. 29, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
110-OCT-2003 (Rel. 42, Last annotation update)
Zinc finger protein 93 (Zinc finger protein HTF34) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17.8%; Score 396.5; DB 1; Length 595; 31.7%; Pred. No. 1.6e-16; ive 48; Mismatches 160; Indels 51
                                                                                                                                   C2H2-TYPE.

C2H2-TYPE.

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C2H2-TYPE.

C2H2-TYPE.

C2H2-TYPE.

C +> Q (IN REF. 2; AAA58671).

R -> I (IN REF. 2; AAA58671).

G -> R (IN REF. 2; AAA58671).

G -> R (IN REF. 2; AAA58671).

M; 44AA0A236D62D43B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68718 MW;
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Best Local Similarity 31.7%
Matches 120; Conservative
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Q05481;
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R GO; GO:000534; C:nucleus; NAS.
R GO; GO:0005370; F:transcription factor activity; NAS.
R GO; GO:0006357; P:regulation of transcription, DNA-dependent; NAS.
R GO; GO:0006355; P:regulation of transcription, DNA-dependent; NAS.
R InterPro; IPR001909; RAB.
R InterPro; IPR001909; ZH=C2H2.
R InterPro; IPR001909; ZH=C2H2.
R Fam; PF00096; ZH=C2H2; 16.
R PRINTS; PR000969; ZHCFNGER.
P PRODOM; PD000003; ZH=C2H2; 7.
R SWART; SM00349; KRAB; 1.
R SWART; SM00349; KRAB; 1.
                                                                                               SEQUENCE OF 1-191 FROM N.A.
MEDLINE-91219421; PubMed-2023909;
Bellefroid E.J., Poncelet D.A., Lecocq P.J., Revelant O.,
Martial J.A.,
"The evolutionarily conserved Kruppel-associated box domain defines a
                                                                                                                                                                                                                   PROSITE; PS50805; KRAB; 1.
PROSITE; PS00028; ZINC_FINGER_C2H2_2; 17.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 17.
Transcription regulation; Zinc-finger; DNA-binding; Metal-binding;
  'Sequence analysis of a 5.7 Mb region in 19p13.1 between OLFR and
                                                Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (DEGENERATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGKGCVGKKGLSSHMLSHDDSTMIKIWTCDYCDVGK-FAKKNELVEHYNIFHDGNIPDDL 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       261 LKETEVKKLENLIDQGSKLNNLHELET--EKLKVEEDEEDEEDEEDS---LDEKRSDVRSDSM 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----HGGSPAYQCDHPGCFKNFQTWSVLQFHIKQSH---PKLKCPK 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       369 ECGKAFIWSSVLTRHKRVHTGEKPYKCEE--CGKAFKYSSTLSSH-KRSHTGEKPYKCEE 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23 KKYICTYEGCDKAYNRPSILLEQHIRTHSNDRPYKCTVDDCDKAFFRKSHLETHIVSHSEK
                                                                                                                                                                                                                                                                                                                                                                                                                                     132 -----ILSVH-----EKTLTCKOCNKVFTRPSKLAOHKLKH------
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Proc. Natl. Acad. Sci. U. S.A. 88:3606.3612(1991).

-! SUBCELLULAR LOCATION: Nuclear (Probable).

-! SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-FINGER PROTEINS.

-!- SIMILARITY: CONTAINS 1 KRAB domain.

-!- SHILARITY: CONTAINS 1 KRAB domain.

-!- CAUTION: THE SEQUENCE PROM POSITION 1159 TO THE C-TERMINAL IS DERIVED FROM THE TRANSLATION OF AN ALU REPEAT.
                                                                                                                     92; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 316 SAQRSIKSFTASLEGSKSVSKLISNSGKKINCPKNNCDRMFSREYDLRRHLKWH 369
                                                                                                                                                                                                                                                                                                        83 KPFHCSVCGKGVNSRQHLKRHEITHT--KSFKCTFENCQEAFYKHQSLRHH-----
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MEDLINES-9223677, PubMed=8467795;

Bellefroid B.J., Marine J.C., Ried T., Lecocq P.J., Riviere M.,

Amemiya C.T., Poncelet D.A., Coulie P.G., de Jong P.J.,

Spirer C., Ward D.C., Martial J.A.,

"Clustered organization of homologous KRAB zinc-finger genes with
enhanced expression in human T lymphoid cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
MCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             534 KCEECGKAF--HLSTHLTTHKILHTGEKPYRC--RECGKAFNHSATLSSHKKIH
                                                         Length 616;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Zinc finger protein 91 (Zinc finger protein HTF10) (HPF7).
2NF91.
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SEQUENCE OF 15-204 FROM N.A.
MEDLINE=91219421; PubMed=2023909;
Bellefroid E.J., Poncelet D.A., Lecocq P.J., Revelant O.,
                                                  Query Match
Best Local Similarity 29.7%; Pred. No. 2.1e-16;
Matches 123; Conservative 42; Mismatches 157; Indels
DF309883AB61160A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1191 AA
70572 MW;
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or send an email to license@lsb-sib.ch).
                                                                                                                        EMBL; L11672; AAA59469:1;

DR RMBL; MG1871; AAA58672:1; ALI_SEQ.

BR RMBL; MG1871; AAA58672:1; ALI_SEQ.

DR PIR; S35305; S35305.

DR PORO47; L2F2.

DR RMM; 603971;

CR GO: 000056370; F:transcription factor activity; NAS.

GO; GO:0006270; F:transcription of transcription, DNA-dependent; NAS.

R GO; GO:0006270; F:transcription of transcription, DNA-dependent; NAS.

R GO; GO:0006370; F:transcription of transcription, DNA-dependent; NAS.

R GO; GO:0006370; F:transcription of transcription, DNA-dependent; NAS.

R GO; GO:0006370; F:transcription of transcription, DNA-dependent; NAS.

R DR COOOCOS; RRAB; L.

R RIMEY; RRO0006; Zf-C2H2; 34.

R PRIMEY; SNO0349; KRAB; L.

R PROSITE; PSCO028; ZINC_FINGER_C2H2_2; 35.

R PROSITE; PSCO028; ZINC_FINGER_C2H2_2; 35.

W TRANSCRIPTION regulation; Zinc_finger; DNA-binding; Metal-binding; M Nuclear protein; Repeat.

M Nuclear protein; Repeat.

PROMATINE PROSITE; PSCO028; ZINC_FINGER_C3H2_2; 35.

W Nuclear protein; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17.7%; Score 393.5; DB 1; Length 1191; 35.8%; Pred. No. 5.2e-16; ive 40; Mismatches 109; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1050 1072 C2H2-TYPE.
1078 1100 C2H2-TYPE.
1106 1128 C2H2-TYPE.
1134 1156 C2H2-TYPE.
1191 AA, 137225 MW; 581056BB11B8716D CRC64,
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C2H2-TYPE (DEGENERATE).
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Conservative

Similarity 98; Conserv

Query Match Best Local S Matches 98

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
                                                                                                                                          961 IGEKPYKCEECGKAFRKSSTLTEHKIIHTGEKPYKC--EECGKAFSQSSTLTRHTRMHTG 1018
                                                                                                                                                                                                                                                                                                                                                                               1075 EKPYKCEECGKAFSQSSTLITRHKRLH---TGEKPYKCGEC--GKAFKESSALIKHKIIHT 1129
                                                                                                                                                                                                                                               137 EKTLICKOCNKVFTRPSKLAQHKLKHHGGSPAYQCDHPGCFKNPQTWSVLQFHIKQSHPK 196
SEKKPFHCSVCGKGVNSRQHLKRHEITHT--KSFKCTFENCQEAFYKHQSL-RHHILSVH 136
                                                                                                                                                                                                                                                                                                                                   197 ---LKCPKCGKGCVGKKGLSSHMLSHDDSTWIKIWTCDYCDVGKFAKKNELVEHYNIFHD
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23.47 HUMAN STANDARD;
28.FEB-2003 (Rel. 41, Last sequence update)
28.FEB-2003 (Rel. 41, Last annotation update)
10.OCT-2003 (Rel. 42, Last annotation update)
210.FEB-2003 (Rel. 42, Last annotation update)
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Marken C.U., Nicholson G.C.;
WRANKL regulated ainc finger protein in osteoclastogenesis.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1130 GE-----KPYKCEKCCKAFNQSSILTNHKKIHT 1157
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EMBL, AL713691; CAD28491.1; --
Genew, HGMC:16447; ZNB347.
InterPro; IPR001909; KRAB.
InterPro; IPR007087; Znf C2H2.
InterPro; IPR007086; Znf C2H2.
InterPro; IPR007086; Znf C2H2.
Fam; PF001352; KRAB; 1.
Pfam; PF00096; Zf CZH2; 18.
PR0DOM; PD000003; ZiNCPINGER.
PRODOM; SMO349; KRAB; 1.
SMART; SM0349; KRAB; 1.
PROSITE; PS50805; KRAB; 1.
PROSITE; PS50805; KRAB; 1.
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70 SHLETHIVSHSEKKPFHCSVCGKGVNSRQHLKRHEITHT--KSFKCTFENCQEAFYKHQS 127
                                                                                                                                                                                                                                                                                                                                                                                                 442 SSLAIHLVIHTGEKPYKCHECGKVFRNSHLARHQLIHTGEKPYKC--NECGKAFRAHSN 499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          557 TTHQVIHTGEKPYKCNECGKVFTQNSHLARHRGIH---TGEKPYKCNEC--GKVFRHNSY 611
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                                                                                                                                                                                                                                                                                                                                       11 SSL-ISSSSSRPKKYICTYEGODKAYNRPSLLEQHLRTHSNDRPYKCTVDDCDKAFFRK
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PROSITE; PSS0157; ZINC FINGER C2H2 2; 20.
Transcription regulation; DNA-binding; Zinc-finger; Metal-binding;
Nuclear protein; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                        Score 387.5; DB 1; Length 839;
Pred. No. 8e-16;
46; Mismatches 154; Indels 53;
                                                                                                                                                                                                                                                                   F7F7CC7069E7844E CRC64;
                                                               C2H2-TYPE (DEGENERATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Z431_HUMAN STANDARD; PRT; 576 AA. 08TF32; QBIWC4; Created) 10-0CT-2003 [Rel. 42, Last sequence update) 10-0CT-2003 [Rel. 42, Last annotation update) 2inc finger protein 431. ZNF413 OR KIAAL969. Home sapiens (Human)
                                                                                                                                                                                                                                                       787 C.
95771 MW;
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R. MEDLINE=22388257; PubMed=12477932;
R. MEDLINE=22388257; PubMed=12477932;
R. Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
R. Altsuner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
R. Altschul S.F., Zeeberg B., Buetcow K.H., Schaefer C.F., Bhat N.K.,
R. Altschul S.F., Zeeberg B., Buetcow K.H., Schaefer C.F., Bhat N.K.,
R. Altschul S.F., Zeeberg B., Buercow K.H., Schaefer C.F., Bhat N.K.,
R. Altschul S.F., Zeeberg B., Buercow K.H., Schaefer C.F., Bhat N.K.,
R. Stapleton M. J. Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
R. Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
R. Anda S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
R. Andas S.N., McEnan K.J., Malek J.A., Gunaratue P.H.,
R. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
R. Antingo M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
R. Bakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
R. Antingo M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
R. Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
R. Goneration and initial analysks of more than 15,000 full-length human
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                                    Nagase T., Kikuno K., Ohara O.;
"Frediction of the coding sequences of unidentified human genes. XXII.
The complete sequences of 50 new CDNA clones which code for large
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50865; REAB; 1.
PROSITE; PS500865; REAB; 1.
PROSITE; PS500257; ZINC FINGER C2H2_1; 12.
PROSITE; PS50157; ZINC FINGER C2H2_2; 13.
Transcription regulation; DNA-binding; Zinc-finger; Metal-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- FUNCTION: May be involved in transcriptional regulation.
-!- SUBCELLULAR LOCATION: Nuclear (Potential).
-!- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C242-TYPE ZINC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (DEGENERATE)
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-!- SIMILARITY: Contains 13 CSH2-type zinc fingers.
-!- SIMILARITY: Contains 13 CSH2-type zinc fingers.
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C2412-TYPE 9 .

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EMBL; BC040506; AAH40506.1; -.
              MEDLINE=21842142; PubMed=11853319;
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InterPro; IPR007087; Znf C2H2.
InterPro; IPR007086; Znf C2H2_sub.
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Pfam; PF00096; zf-C2H2; 12.
PRINTS; PR00048; ZINCFINGER.
SMART; SM00349; KRAB; 1.
SWART; SM00355; ZNF_CZH2; 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genew; HGNC:20809; ZNF431.
                                                                                                             DNA Res. 8:319-327 (2001).
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SEQUENCE FROM N.A.
TISSUE=Testis;
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55; Mismatches 133; Indels
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Matches 109;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       437 FNRSPQLTAHKIIHTGE-----KPYKCEECGKAFSQSSILTT-------473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           299 EEDSLDEKRSDVRSDSMSAQRSIKSFTASLEGSKSVSKLISNSGKKINCPKUNCDRMFSR 358
                                                                                                                                                                                                                                                                                                                                                                         PYKHOSL-RHHILSVHEKTLTCKOCNKVFTRPSKLAQHKLKHHGGSPAYQCDHPGCFKNF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          382 NWSSTLTKHKRIHTGEKPYKCEVCGKAFNESSNLTTHKMIH----TGEKPYKCEEC--GKA 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----HKRIHTGEKPYKCEECGKAFNRSSNLTK--HKIIHTGEKSYKC--EECGKAFNQ 523
                                                                                                                                                                                                                                                                                             KSPCMLLHLSQHKRIHIRENSYQC--EECGKAFKWFSTLTRHKRIHTGEKPFKC--EECG 266
                                                                                                                                                                                                                                                                                                                                          KAFFRKSHLETHIVSHSEKKPFHCSVCGKGVNSRQHLKRHEITHT--KSFKCTFENCQEA 121
                                                                                                                                                                                                                                              KSISSLISSSSS----RPKKYICTYEGCDKAYNRPSLLEOHLRTHSNDRPYKCTVDDCD 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. Krummel G.K., Kvikstad E., Grable L., de Y., Krodoylanni V., de Y., Krummel G.K., Kvikstad E., Gleen A.S., Smith L.M.; Severin J., Gordon L., Shannon M., Brower A., Oleen A.S., Smith L.M.; "Sequence analysis of a 1Mb region in 19q13.2 containing a zinc finger
                                                                                                                                                                                                  Gaps
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Shannon M., Branscomb B., Hauser L., Gordon L., Ashworth L.,
                                                                                                                                                  Length 576;
                                                                                                                                          . Score 385; DB 1; Length 57; Pred. No. 7.5e-16; A8; Mismatches 158; Indels
478 C2H2-TYPE 11.
506 C2H2-TYPE 12.
534 C2H2-TYPE 13.
1198 H -> R (IN REF. 2).
67216 MW; 532774BF69EC9E2A CRC64;
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-!- SIMILARITY: Contains 1 KRAB domain.
-!- SIMILARITY: Contains 17 C2H2-type zinc fingers.
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29.4%;
                                                                                                                                                                                                  Matches 109; Conservative
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ZNF228.
                                               512
198
176 AA;
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R RASP; PO8047; 1SP2.
R GROW, HGWC:13021; ZNF228.
R GROW, HGWC:13021; ZNF228.
R InterPro; IPR001909; KRAB.
R InterPro; IPR007087; Znf_C2H2.
R InterPro; IPR007087; Znf_C2H2.
R Pfam; PF00196; Zf_C2H2; 1.
R Pfam; PF00196; Zf_C2H2; 1.
R PROMOS; Znf_C2H2; 12.
R RMART; SW00349; KRAB; 1.
R SWART; SW0035; Znf_C2H2; 13.
R RASP; SSS0905; KRAB; 1.
R ROSITE; PSS0905; KRAB; 1.
R ROSITE; PSS0197; ZINC_FINGER_C2H2 1; 13.
R ROSITE; PSS0197; ZINC_FINGER_C2H2 2; 17.
R RASCRIPE; PSS0197; ZINC_FINGER_C2H2 2; 17.
R RASCRIPE; PSS0197; ZINC_FINGER_C2H2 2; 17.
R RASCRIPE; PSS0197; ZINC_FINGER_C2H2 2; 17.
R RASCRIPE; PSS0197; ZINC_FINGER_C2H2 2; 17.
R RASCRIPE; PSS0197; ZINC_FINGER_C2H2 2; 17.
R RASCRIPE; PSS0197; ZINC_FINGER_C2H2 2; 17.
R RASCRIPE; PSS0197; ZINC_FINGER_C2H2 2; 17.
R RASCRIPE; PSS0197; ZINC_FINGER_C2H2 2; 17.
R RASCRIPE; PSS0197; ZINC_FINGER_C2H2 2; 17.
R RASCRIPE; PSS0197; ZINC_FINGER_C2H2 2; 17.
R RASCRIPE; PSS0197; ZINC_FINGER_C2H2 2; 17.
R RASCRIPE; PSS0197; ZINC_FINGER_C2H2 2; 17.
R RASCRIPE; PSS0197; ZINC_FINGER_C2H2 2; 17.
R RASCRIPE; PSS0197; ZINC_FINGER_C2H2 2; 17.
R RASCRIPE; PSS0197; ZINC_FINGER_C2H2 2; 17.
R RASCRIPE; PSS0197; ZINC_FINGER_C2H2 2; 17.
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NCBI TaxID=9606;
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                                       258 DOLLKETEVKKLENILLDQGSKLNNLHELETEKLKVEEDEEDEEDSLDEKRSDVRSDSMSA 317
 ICEVCGKGFSQRAYLQGHQRVH---TRVKPYKCEMCGKG-FSQSSRLEAHRRV-HTGGKP 776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------YKCE-VCTKGFS-----ESSRLQAHQ------RVHVEGRPYKC
                                                                                                                               PROSTIE; PSS0805; KĒAB; 1.
PROSTIE; PSS0805; KĒAB; 1.
PROSITE; PS00128; ZINC_FINGER_C2H2_2; 12.
Transcription regulation; DNA-binding; Zinc-finger; Metal-binding;
                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                             318 QRSIKSFT--ASLEGSKSVSKLISNSGKK-INCPKNNCDRMFSREYDLRRHLKWH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bi A., Yu L.;
"Homo sapiens mRNA similar to zinc finger protein 85.";
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                       2998GI; Q86V70;
10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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C2H2-TYPE 1.
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InterPro; IPR001089; Znf_C2H2.
Pfam; PF01322; KRAB; 1.
Pfam; PF00096; Zf_C2H2; 3.
SPCDOm; PD000003; Znf_C2H2; 3.
SWART; SM00349; KRAB; 1.
SMART; SM00355; ZnF_C2H2; 3.
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                                                                                                                                                                                                                                             STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           287 KPYRC--EECGKTFNRSSHLTTHKRIHTGEKPYRC--EEGGRAFNRSSHLTTHKIIHTGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83 KPFHCSVCGKGVNSRQHLKRHEITHT--KSFKCTFENCQEAFYKHQSL-RHHILSVHEK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUB=placenta;
MEDLINE=97230463; PubMed=9073517;
Goldwurm S., Menzies M.L., Banyer J.L., Powell B.L.W.,
Jawinska E.C.;
"Identification of a novel Krueppel-related zinc finger gene (ZNF184)
mapping to 6p21.3 ";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        139 -----TLT----TLT----CKQCNKVFTRPSKLAQHKLKHHGGSPAYQC
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Mammalia, Butheria, Primates; Catarrhini, Hominidae, Homo.
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Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases
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2184 HUMAN STANDAN-...
2185-710-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
- ^m-2003 (Rel. 42, Last annotation update)
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449 AE--CGKSFSYWSSLAQHLKIHTGEKPYKCNECGKAFSYCSSLTQHRRIHTREKPFECSE
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                                                                                 YKCNECGKAFNGPSTFIRHEMIHTGEKPYECNECGKAFSQHSNLTQHQKTHTGEKP-YDC
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                                                      ------LRHHILSVHEKTLTCKQCNKVFTRPSKLAQHKLKHHGGSPAYQC
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conservation of the Xenopus
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Lee M.S., Gippert G.P., Soman K.V., Case D.A., Wright P.E.;
"Three-dimensional solution structure of a single zinc finger DNA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xenopus laevis (African clawed frog).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoldea, Pipidae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEBS Lett. 254:159-164(1989).
-!- FUNCTION: BINDS RNA. COULD FUNCTION IN POST-TRANSLATIONAL
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MEDLINE=B8082679; PubMed=2826129;
Ruiz i Altaba A., Perry-O'Keefe H., Melton D.A.;
"Xfin: an embryonic gene encoding a multifingered protein
                                                                                                                                                                                                                                                                                     -----DDTLKETEVKKLE---NLLDQGSKLN-NLHELETEKL-
                                                                                                                                                                                                                                                                                                                                                                                            621 KAFRHCSSLAQHQKTHTBEKPYQCNKCEKTFSQSSHLTQHQR-
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01-AUG-1988 (Rel. 08, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
XFIN.
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Andreazzoli M., de Lucchini S., Costa M.,
KRA binding properties and evolutionary c
multifinger protein Xfin.";
Nucleic Acids Res. 21:4218-4225 (1993).
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                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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WIM, 602277;

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; Pred. No. 3.4e-15;
52; Mismatches 146; Indels 140; Gaps
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Local Similarity 25.2%;
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Matches 119;
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 REGULATION PROCESSES.
SUBCELLULAR LOCATION: Cytoplasmic.
TISSUE SPECIFICITY: OOCYTES AND IN SPECIALIZED CELL TYPES SUCH
                                                  PTM: Phosphorylated.
SIMILARITY: DEDNOS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-FINGER PROTEINS.
SIMILARITY: Contains 1 KRAB domain.
                                                                                                                                                               InterPro; IPR007087; Znf_C2H2.

Pfam; PF0132; KRAB; 1.

Prom; PF000803; Znf_C2H2; 36.

Probom; PD000003; Znf_C2H2; 20.

SMART; SM00349; XRAB; 1.

SMART; SM0035; Znf_C2H2; 35.

PROSITE; PS00028; ZINC_FINGER C2H2_1; 35.

PROSITE; PS0157; ZINC_FINGER_C2H2_2; 37.

Zinc_finger; Metal-binding; RNA-binding; Repeat; 3D-structure; Phosphorylation.
                             AND
                      AS NEURAL RETINA CONES.
DEVELOPMENTAL STAGE: EXPRESSED THROUGHOUT OOGENESIS
                                           CONTAINS 37 FINGER MOTIFS IN 6 DOMAINS
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                                                                                                                                                       Interpro; IPR001909; KRAB.
Interpro; IPR007087; Znf_C2H2.
                                                                                                                                          EMBL; X06021; CAA29425.1; -. PDB; 12NF; 15-0CT-91.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 321 IKSFTASLEGSKSVSKLISNSGKK-INCPKNNCDRMFSREYDLRRHLKWHD-DNLQRIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           454 ILHQRIHTGERPYKCTLCDRTFIQNSDLVKHQKVHANLPLSDPHTANSPHKCSK--CDLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STMIKIW------TCDYCDVGKFAKKNELVEHYNIFHDGNIPDDLLKETEVKKLENL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             624 FIQKSAL -----TKHSRTHTGEKPYPCTQCGKSFIQNSDLVKHORIHTGEKPYHCTEC
                                                                                                                                                                                                                                   SSLISSSSSRPKKYICTYEGCDKAYNRPSLLEQHLRTHSNDRPYKCTVDDCDKAFFRKS
                                                                                                                                                                                                                                                                                                                                                                            71 HLETHIVSHSEKKPFHCSVCGKGVNSRQHLKRHEITHT--KSFKCTFENCQEAFYKHQSL
                                                                                                                                                                                   Gaps
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J. Biol. Chem. 274:35741-35748(1999).
-:- FUNCTION: May function as a transcription factor.
-:- SUBCELLULAR LOCATION: Nuclear (Probable).
-:- SIMILARITY: BELONGS TO THE KRUPPEL FAMILY OF C2H2-TYPE ZINC-FINGER PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                81;
                                                                                                                       Length 1350;
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16-0cT-2001 (Rel. 40, Last sequence update)
10-0cT-2003 (Rel. 42, Last annotation update)
2inc finger protein 257 (Bone marrow zinc finger 4) (BMZF-4)
ZNF257 OR BMZF4.
                                                                          155804 MW; 27F10AB0851E0AD8 CRC64;
                                                                                                                             16.8%; Score 375.5; DB 1; 27.3%; Pred. No. 6.8e-15; ive 65; Mismatches 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         535 AA
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MEDLINE=20054457; PubMed=10585455;
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                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123 YKHQSL----RHHILSVHEKTLTCKQCNKVFTRPSKLAQHKLKHHGGSPAYQCDHPGCFK 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         149 KYVKVFYKFSNSDRHKIRHTEKKICKCKECGKĀPNQSSALTRHKMTHTGEKPYKC--EEC 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DKAFFRKSHLETHIVSHSEKKPFHCSVCGKGVNSRQHLKRHEITHTKSFKCTFENCQEAF 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                179 NFQTWSVLQFHIKQSHPK---LKCPKCGKGCVGKKGLSSHMLSHDDSTMIKIWTCD-YCD 234
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                                                                                                                                                    CC EMBL, AF070651; AAD20957.1; -.

BR HSSF; P08047; 1SF2.

BR ROSS POROGAT; 1SF2.

DR MIN; 606097; -.

BR GO, GO:0003677; F:DNA binding; NAS.

GO, GO:000357; F:DNA binding; NAS.

GO, GO:000355; P:regulation of transcription, DNA-dependent; NAS.

BR GO, GO:0008255; P:regulation of transcription, DNA-dependent; NAS.

BR GO, GO:0008255; P:regulation of transcription, DNA-dependent; NAS.

BR GO; GO:0008255; P:regulation of transcription, DNA-dependent; NAS.

BR FERN, FF001909; KRAB; 1.

BR FERN, FF00096; ZIC_C2H2.

BR RAINTS; PRO0046; ZINCFINGER.

BRAINTS; ROWO349; KRAB; 1.

BRAZT; SW00349; KRAB; 1.

BRAZT; SW00355; ZIC_C2H2; 9.

BR PROSITE; PS50805; KRAB; 1.

BROSITE; PS50805; KRAB; 1.

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Search completed: May Job time : 19 secs

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May 5, 2004, 15:19:16 ; Search time 20 Seconds (without alignments) 1981.545 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                       OM protein - protein search, using sw model
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US-09-831-804-3 2229 1 MSESDETKSISSLISSSSSPLVKKARMDLLPNETSVISR 412 BLOSUM62 Gapop 10.0 , Gapext 0.5 Title: Perfect score: Sequence: Scoring table:

283366 Total number of hits satisfying chosen parameters: 283366 seqs, 96191526 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	fac	rote	zinc finger protei	rep	d bu	rot	er protein -	finger	nger prote	protein	protein	iption f	protein 1,	protein (krueppel-related p	nger prote	×	ote	finger protein (cl	ı	tic	cal pr	prote	spermatogenesis pr	nger pro	inger protein H	er protein	evelopment	on f
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S10245 S47070	C32891 A46830 I38600	JC7779 S22954	S03677 S06572 S06548	T14757 S59069 S47073	T08674 I38598 A54603
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ALIGNMENTS

	transcription factor IIIA - yeast (Saccharomyces cerevisiae) transcription factor IIIA - yeast (Saccharomyces cerevisiae) Althernate names: protein P9677.9; protein YPR186c; TFC2 protein C;Species: Saccharomyces cerevisiae C;Date: 16-Sep-1992 #sequence_revisiae C;Date: 16-Sep-1992 #sequence_revisiae C;Date: 16-Sep-1992 #sequence_revisian C;Accession; S20050; Ad086; SSB316 C;Accession; B.; Friesen, J.D.; Segall, J. J. Biol. Chem. 267, 3282-3288, 1992 A;Title: The deduced sequence of the transcription factor TFIIIA from Saccharomyces cerevisites number: S20050; MUID:92147684; PMID:1737784 A;Accession: S20050;	A; Wolecule type: DNA A; Residues: 1-429 < ARC. A; Residues: 1-429 < ARC. A; Cross-references: 1-429 < ARC. A; Cross-references: 1-429 < ARC. B; Cross-references: 1-429 < ARC. B; Cross-references: 1-429 < ARC. B; Cross-references: 1-429 < ARC. B; Cross-references: 1-44086; WID: 92237295; PMID: 1570325 A; Accession: A44086 A; Accession: A44086 A; Accession: A44086 A; Accession: A44086 A; Accession: A44086 A; Accession: A44086 A; Accession: A44086 A; Accession: A44086 A; Accession: A44086	A.Cross-references: GB.M90638 R.Miller, N. Submitted to the EMBL Data Library, April 1995 A.Description: The sequence of S. cerevisiae cosmid 9677. A.Accession: S58816 A.Accession: S58816 A.Mocession: S58816 A.Mocession: S58816 A.Mocession: S58816 A.Mocession: S58816 A.Mocession: S58816 A.Mocession: S58816 A.Mocession: S58816 A.Mocession: S58816 A.Mocession: S58816 A.Mocession: S6881	37.6%; Score 837.5; DB 2; Length 429; ; Conservative 62; Mismatches 135; Indels 27; Gaps 11; MSESDETKSISSLISSSSSRPKKYICTYEGCDKAYNRPSLLEQH-LRTHSNDRPYKC 57 : : : :
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137676
210-6110ger protein - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec.1999 #sequence_revision 03-Dec-1999 #text_change 01-Dec-2000
C;Date: 03-Dec.1999 #sequence_revision 03-Dec-1999 #text_change 01-Dec-2000
C;Date: 03-Dec.1999 #sequence_revision 03-Dec-1999 #text_change 01-Dec-2000
C;Date: 03-Dec.1999 #sequence_revision 03-Dec-1999 #text_change 01-Dec-2000
C;Date: 03-Dec.1999 #sequence 01-Dec-2000
R;Mcocession: T37676
A;Reference number: 221736
A;Reference number: 221736
A;Residues: 1-374 cMCD>
A;Coss-references: EMBL:AL132675; PIDN:CAB59689.1; GSPDB:GN00066; SPDB:SPAC144.09c
A;Experimental source: strain 972h-; cosmid c144
C;Genetics:
A;Genetics:
A;Mat position: 1
A;Mat position: 1
A;Mat position: 1
A;Mat position: 1
A;Mat cons: 50/3
C;Superfamily: zinc finger protein ZFP-36; LIM metal-binding repeat homology
                                  235
                                                                                                                                          312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           309 IEGVAIHDQKEKELSSNLVSDVAKKIINEVTG--HGYK-----EAREYSCSFPECNY 358
141 CNLRFYKHPQLRAHILSVHLHKLTCPHCNKSFQRPYRLRNHISKHHDPEVBNPYQCTFAG 200
                                                       201 CCKEFRIWSQLQSHIKNDHPKLKCPICSKPCVGENGLQMHMIHDDSLVTKNWKCHICPD 260
                                                                                                      236 GKFAKKNELVEHYNIFH-DGNIPDDL-LKETEVKKLENLLDQGSKLNNLHELETEKLKVE 293
                                                                                                                                                                             EDEEDEEDSLDEKRSDVRSDSMSAQRSIKSFTASLE-GSKSVSKLISNSGKKINCPKNNC 352
                                                                                                                                                                                                      133 HISACHTHLLPYPCTYQDCELRPATKOKLQNHVNRAHEKIISYSCPHESCVGHEGFEKWS 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         185 VLQFHIKQSHPKLKCPKCGKGCVGKKGLSSHMLSHDDSTMIKIWTCDYCDV----GKFAK 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72
                                                                                                                               261 MSFSRXHDLLTHYGSIHTBEDIPLELKYKISDIQQL--VQDHGVQLGN-----SKHSNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 KNELVEHYNIFHDGNIP---DDLLKETEVK-KLENLLDOGSKLNNLHELETEKLKVEEDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75 HIVSHSEKKPFHCSV--CGKGVNSRQHLKRHEITH--TKSFKCTFENCQEAFYKHQSLRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    131 HILSVHEKTL----TCKQCNKVFTRPSKLAQHKLKHHGGSPAYQCDHPGC--FKNFQTWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 SSSSSSRPKKYICTYEGCDKAYNRPSLLEQHLRTHSNDRPYKCTVDDCDKAFFRKSHLET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EDEEDSLDEKRSDVRSDSMS--AQRSIKSFTASLEGSKSVSKLISNSGKKINCPKNNCDR
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22.2%; Score 495; DB 2; Length 374,
Best Local Similarity 32.8%; Pred, No. 5.7e-23;
Matches 123; Conservative 58; Mismatches 160; Indels
                                                                                                                                                                                                                                                                          353 DRMFSREYDLRRHL---KWHDDNLQRIESFLNSIEKEE 387
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expressed in lymphoid cell
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A;Status: preliminary
A;Residues: 1-803 «LOV>
A;Cress-references: EMBL:XS9244; NID:g38031; PIDN:CAA41932.1; PID:g38032
A;Cross-references: EMBL:XS9244; NID:g38031; PIDN:CAA41932.1; PID:g38032
B;Thiesen, H.J.
New Biol. 2, 363-374, 1990
A;Tritle: Multiple genes encoding zinc finger domains are expressed in human T cells.
A;Reference number: 137949; MUID:91145339; PMID:2288909
A;Reference number: 137949; MUID:9145339; PMID:2288909
A;Reference type: mRNA
A;Residues: 476-511 «THI»
A;Residues: 476-511 «THI»
A;Cross-references: EMBL:X52358; NID:g34160; PIDN:CAA36584.1; PID:g930090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Gene: GDB:ZNP43; HTF6
A,GCTOSS-references: GDB:128653
A,Map postition: 19p13.1-19p3
C,Superfamily: zinc finger protein ZFP-36; LIM metal-binding repeat homology
C,Keywords: DNA binding; zinc finger
Zinc finger protein ZNF43 - human
NyAlternate names: zinc finger protein kox27
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: $26823; 137967; $10416
R;Lovering, R.; Trowsdale, J.
Nucleic Acids Res. 19, 2921-2928, 1991
A;Title: A gene encoding 22 highly related zinc fingers is expressed in lymp.
A;Reference number: $26823; MUID:91279444; PMID:1711675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DDCDXAFFRXSHLETHIVSHSEKKPFHCSVCGKGVNSRQHLKRHEITHT - KSFKCTFEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SESDETKSISSLISSSSS--SRPKKYICTYEGCDKAYNRPSLLEQHLRTHSNDRPYKCTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COBAPYKHOSL-RHHILSVHEKTLTCKOCNKVFTRPSKLAQHKLKHGGSPAYQCDHPGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PKNFQTWSVLQFH--IKQSHPKLKCPKCGKGCVGKKGLSSHMLSHDDSTMIKIWTCDYCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VGK-FAKKNELVEHYNI FHDGNI PDDLLKETEVKKLENLLDQGSKLNNLHELETEKLKVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 803;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
17.9%; Score 400; DB 2; Length 803
Best Local Similarity 31.9%; Pred. No. 7.5e-17;
Matches 121; Conservative 53; Mismatches 171; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCDRMFSREYDLRRHLKWH 369
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zinc finger protein ZNF91 - human
C.Species: Homo sapiens (man)
C.Date: 31-Dec-1993 #sequence_revision 02-Jun-1994 #text_change 05-Nov-1999
C.Accession: S35303
R.Bellefroid, B.J.; Marine, J.C.; Ried, T.; Lecocq, P.J.; Riviere, M.; Amemiya, C.; Poncf
ENBO J. 12, 1363-1374, 1993
A.Title: Clustered organization of homologous KRAB zinc-finger genes with enhanced expres
A.Reference number: S35305; MUID:93223677; PMID:8467795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: mRNa
A;Residues: 1-1131 -REL>
A;Cross-references: EMBL:L11672; NID:g186773; PIDN:AAAS9469.1; PID:g186774
A;Note: the authors translated the codon GCA for residue 750 as Thr and GCT for residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1019 EKPYKCEECGKAFNRSSKLTTHKIIHTGEKP-YKCEE--CGKAFISSSTLNGH-KRIHTR 1074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           197 --- LKCPKCGKGCVGKKGLSSHMLSHDDSTMIKIWTCDYCDVGKFAKKNELVEHYNIFHD 253
               TKSFKÇTFENCQEAFYKHOSLR-HILLSVHEKTLTCKQ--CNKVFTRPSKLAQHKLKHHG 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                127 QKQYICSFEDCKKTFKKHQQLKIHQCQHTNEPLFKCTQEGCGKHFASPSKLKRHAKAHEG
                                                                                                                                                  ----YVC-QKGCSFVAKTWTELLKHVRETHKBEILCEVCRKTFKRKDYLKQHMKTHAPER
                                                                                                                                                                                                       --LKCPK--CGKGCVGKKGLSSHMLS-HDDSTMIKIWTCDYCDVGK-FAKKNELVEHYNI
                                                                                                                                                                                                                              SEKKPFHCSVCGKGVNSRQHLKRHEITHT--KSFKCTFENCQEAFYKHQSL-RHHILSVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EKTLTCKQCNKVFTRPSKLAQHKLKHGGSPAYQCDHPGCFKNPQTWSVLQFHIKQSHPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 SRPKKYICTYEGCDKAYNRPSILEQHLRTHSNDRPYKCTVDDCDKAFFRKSHLETHIVSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                 GSPAYQCDHPGCFKNFQTWSVLQFHIKQSHPK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
17.7%; Score 393.5; DB 2;
Best Local Similarity 35.8%; Pred. No. 2.8e-16;
Matches 98; Conservative 40; Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1130 GE-----KPYKCEKCCKAFNQSSILTNHKKIHT 1157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 254 GNIPDDLLKETEVKKLENLLDQGSKLNNLHELET 287
                                                                                                                                                                                                                                                                                                                                      298 VHD----PDKKKMKLKVKK 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A)Gene: GDB:ZNF91; HPF7; HTF10
A;Cross-references: GDB:132284
A;Map position: 19p12-19p12
C;Keywords: DNA binding; zinc finger
                                                                                                                                                                                                                                                                                                        FHDGNIPDDLLKETEVKK 268
                                                                                                                                                                                                                                                                                                        251
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C,Species: Homo sapiens (man)
C,Species: Homo sapiens (man)
C,Bate: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C;Bate: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C;Bate: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C;Bate: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C;Bate: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
R;Bate: 159, 215-218, 1995
R;Date: 199, 215-218, 1995
A;Title: Cloning and expression analysis of a human cDNA homologous to Xenopus TFIIIA.
A;Reference number: 138937; MUID:95347600; PMID:7622052
A;Reference number: 138937; MUID:95347600; PMID:7622052
A;Residues: 1-363 exRes
A;Residues: 1-363 exRes
A;Residues: 1-363 exRes
A;Residues: 1-363 exRes
A;Cross-references: EMBL:U20272; NID:9644870; PIDN:AAA75623.1; PID:9644871
C;Superfamily: transcription factor IIIA
                                                                                                                                                                                                                                                                                                                              17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69 KSHLETHIVSHSEKKPFHCSVCGKGVNSRQHLKRHEITHT--KSFKCTFENCQEAFYKHQ 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       127 SL-RHHILSVHEKTLTCKQCNKVFTRPSKLAQHKLKHHGGSPAYQCDHPGCFKNFQTWSV 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        300 TLTTHRKIHTGEKPYRCEEGGRAFKQSSNLTTHKIHTGERP-YRCKK--CGRAFNQSAH 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  244 LVEHYNIFHDGNIPDDLLKETEVKKLENLLDQGSKLNNLHELETEKLKVEEDBEDDEDSL 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                304 DEKRSDVRSDSMSAQRSIKSFTASL-----EGSK----SVSKLISNSGKKINCPKN 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53
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                                                                                                                                                                                                                                                                                                                                                                                 68
                                           A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: mRNA
A/Rosidues: 1-595 <PON>
A/Molecule sessions: 1-595 <PON>
A/Rosidues: 1-595 <PON>
C/Genetics: PBBL:U35376; NID:g1017721; PIDN:AAA79179.1; PID:g1017722
C/Genetics: A/Gene: GDB:I3279
A/Cross-references: GDB:13279
A/Map position: 19p12-19p12
C/Superfamily: zinc finger protein ZFP-36; LIM metal-binding repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                        LOFH - - I KOSH PKLKCPKCGKGCVGKKGLSSHMLSHDDSTMIKIWTCDYCDVGKFAKKNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 412 TLTKHKIIHTGE-----KPYKSKECEKAFNQSSKL------TEHKKIHTGEKPYE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PYKCTVDDCDKAFFRKSHLETHIVSHSEKKPFHCSV--CGKGVNSRQHLKRH-EITH---
                                                                                                                                                                                                                                                                                                                                                                              10 ISSLISSSS-SSRPKKYICTYEGCDKAYNRPSLLEQHLRTHSNDRPYKCTVDDCDKAFFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----PKKYICTYEGCDKAYNRPSLLEQHLRTHSNDR
                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                      Length 595;
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17.7%; Score 395.5; DB 2;
Best Local Similarity 31.1%; Pred. No. 5.9e-17;
Matches 99; Conservative 54; Mismatches 96;
                                                                                                                                                                                                                                                                                 Query Match 17.8%; Score 396.5; DB 2; Best Local Similarity 31.7%; Pred. No. 8.8e-17; Matches 120; Conservative 48; Mismatches 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            514 ECGKAFNQSSKLTKHKKIH 532
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A; Reference number: G09169
A; Accession: G02075
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14868

zinc finger protein 51 - mouse

N.A.Lernace names: finger protein zfeci2

C.Species: Was musculus (house mouse)

C.Species: Was musculus (house mouse)

C.Species: Was musculus (house mouse)

C.Species: Musculus (house mouse)

C.Species: Musculus (house mouse)

C.Species: Musculus (house mouse)

C.Species: Musculus (house mouse)

C.Species: Musculus (house mouse)

C.Species: Musculus (house mouse)

C.Species: Musculus (house mouse)

R.Burke, P.S.; Don, J.; Wolgemuth, D.J.

Mam. Genome 5, 387.389, 1994

A.Reference number: 148668; MulD:94319090; PMID:8043957

A.Reference number: 148668; MulD:94319090; PMID:8043957

A.Molecule type: mRMA

A.Residues: 1.710 CRES.

A.Cross-references: EMBL:X74855; NID:9488832; PIDN:CAA52847.1; PID:9488833

R.Cross-references: EMBL:X74855; NID:9488832; PIDN:CAA52847.1; PID:9488833

R.Cross-reference number: A40984; MulD:91376058; PMID:1680234

A.Accession: A40984

A.Scatus: preliminary

A.Molecule type: mRNA

A.Residues: 672-710 CRO>

A.Residues: 672-710 CRO>

A.Cross-references: GB:M74235

C.Genetics:
                A/Accession: S00647
A/Molecule type: mRNA
A/Residues: 1-1350 cRUI>
A/Cross-references: EMBL:X06021
A/Note: it is uncertain whether Met-1, Met-11, Met-16, Met-38, or Met-39 is the initiato
C/Genetics:
A/Gene: fin
C/Keywords: DNA binding; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                       340 SFLNHQQTHSREKPYLCSH--CNKGFIQNSDLVKHFRTHTGERPYQCA--ECHKGFIQKS 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                           71 HLETHIVSHSEKKPFHCSVCGKGVNSRQHLKRHEITHT--KSFKCTFENCQEAFYKHQSL 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               396 DLVKHLRTHTGEKPFKCSHCDKKFTERSALAKHQRTHTGEKPYKCS--DCGKEFTQRSNL 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               129 -RHHILSVHEKTLTCKQCNKVFTRPSKLAQHKLKH------HGGSPAYQCDHPGCFKN 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      512 FSHWSTFMKHSGEKKEÇCAECKKGFTQKSDLVKHIRVHTGEKPFKCLLCKKSFSQN 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STMIKIW-------TCDYCDVGKFAKKNELVEHYNIFHDGNIPDDLLKETEVKKLENL 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         572 SDLHKHWRIHTGEKPFPCYTCD-KSFTERSALIKHHRT-HTGERPH-----KCSVCQKG 623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         273 LDQGSKLNNLHELETEKLKVEEDEEDELDEKRSDVRSDSMSAQR-----S 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          624 FIQKSAL-----TKHSRTHTGEKPYPCTQCGKSFIQNSDLVKHQRIHTGEKPYHCTEC 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          677 NKRFT---EGSSLVKHRRTHSGEKPYRCPQ--CEKTFIQSSDLVKHLVVHNGENPPAATA 731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                454 ILHORIHTGERPYKCTLCDRTFIQNSDLVKHOKVHANLPLSDPHTANSPHKCSK--CDLT 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 321 IKSFŢASLEGSKSVSKLISNSGKK-INCPKNNCDRMFSREYDLRRHLKWHD-DNLQRIES 378
                                                                                                                                                                                                                                                                                                                                                           11 SSLISSSSSRPKKYICTYEGCDKAYNRPSLLEQHLRTHSNDRPYKCTVDDCDKAFFRKS 70
                                                                                                                                                                                                                                                  Query Match
16.8%; Score 375.5; DB 2; Length 1350;
Best Local Similarity 27.3%; Pred. No. 4e-15;
Matches 119; Conservative 65; Mismatches 171; Indels 81; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180 FQTWSVLQFHIK--QSHPKLKCPKCGKGCVGKKGLSSHMLSH-----
A; Reference number: S00647; MUID:88082679; PMID:2826129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  379 FLN-SIEKEETPEGEP 393
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CiSpecies: Homo sapiens (man)
CiDate: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 01-Dec-2000
CiDate: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 01-Dec-2000
CiDates 102-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 01-Dec-2000
Riftrance, A. Archidiacono, N.; Rocchi, M.; Marino, M.; Grimaldi, G.
Genomics 9, 728-736, 1991
A;Title: Isolation and expression analysis of a human zinc finger gene (ZNP41) located on A;Reference number: A54661; MUID:91244317; PMID:2037297
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A;Cross-references: GB:M35548; GB:M92443; NID:g340443; PIDN:AAA61312.1; PID:g340444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        367 YKCRECDKSFIHSSHIRRHQNVHTGERPYRC--KECDKSPHESATLAEHEKSHTGEKTYK 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       425 CRECDKSFTQRAYLRNHHNRVHTGERPYECKE--CGKSFTTCSTLRIHQT1HTGKKPYKC 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85 FHCSVCGKGVNSRQHLKRHEITHT--KSFKCTFENCQEAFYKHQSLRHHILS-VHEKTLT 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    142 CKQCNKVFTRPSKLAQHKLKHHGGSPAYQCDHPGCFKNFQTWSVLQFH--IKQSHPKLKC 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           200 PKCGKGCVGKKGLSSHMLSHDDSTMIKIWTCDYCDVGKFAKKNELVEHYNIPHDGNIPDD 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               483 IECGKSFTNNSYLRTHQKVHSGE---KPYRCKECD-KSFTSCSTLKAHQSI-HTGEKPYK 537
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LKIH-QKSHIGERHYECKDCGKAFIQKSTLSVHQRIH---TGEKPYVCPEC--GKAFIQK 382
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                                                                                                                                                186 LQFHIKQSH---PKLKCPKCGKGCVGKKGLSSHMLSHDDSTMIKIWTCDYCDVGK-FAKK 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25 YIÇTYEGCDKAYNRPŞLLEQHLRTHSNDRPYKCTVDDCDKAFFRKSHLETHIVSHSEKKP 84
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A;Gene: Zfp-51
C;Superfamily: zinc finger protein ZFP-36; LIM metal-binding repeat homology
C;Keywords: DNA binding; zinc finger
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C;Superfamily: zinc finger protein ZFP-36; LIM metal-binding repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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16.7%; Score 373; DB 2; Length 542;
Best Local Similarity 29.0%; Pred. No. 2.1e-15;
Matches 115; Conservative 59; Mismatches 156; Indels 66; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          320 SIKSFTASLEGSKSVSKLISNSGKK-INCPKNNCDRMFSREYDLRRHLKWH 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            584 KI-------HSGEXPYKC--RDCDISFSQISNLRRHQKLH 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53;
                                                                                                                                                                                                                                                                                                       Query Macch 16.8%; Score 374.5; DB 2; Length 710; Best Local Similarity 29.6%; Pred. No. 2.38-15; Macches 104; Conservative 54; Mismatches 140; Indels 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              zinc finger protein ZNF41 - human (fragment)
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A;Cross-references: GDB:125865; OMIM:314995
                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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C;Accession: UN0533
R;Brady, J.P.; Piatigorsky, J.
R;Brady, J.P.; Piatigorsky, J.
A;Brady, J.P.; Piatigorsky, J.
A;Title: Cloning and characterization of a novel zinc-finger protein encoding cDNA from A;Reference number: JN0533; MUID:93185925; PMID:8444344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LDEKRSDVRSDSMSAQRSIKSFTASLEGSKSVSKLIS----NSGKK-INCPKNNCDRMFS 357
                                                                                                                                                                                                                                                                                                                                   A;Accession: UN0533
A;Molecule type: mRNA
A;Residues: 1-393 --6RRA-
A;Cross-references: GB:MN8502; NID:g200406; PIDN:AAA39949.1; PID:g200407
A;Cross-references: GB:MN8502; NID:g200406; PIDN:AAA39949.1; PID:g200407
A;Experimental source: eye lens
C;Superfamily: zinc finger protein ZFP-36; LIM metal-binding repeat homology
C;Keywords: DNA binding; eye lens; zinc finger
F;1-62/Region: acidic
F;63-391/Region: zinc finger
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NyAlternate names: TFIIIA
C)Species: Homo sapiens (man)
C)Species: L-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 05-Nov-1999
C)Accession: G01496
R)Becker, K.G.
R)Becker, K.G.
A)Reference number: G07520
A)Reference number: G07520
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A)Refere
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 01-Dec-2000
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A,Cross-references: EMBL:U14134; NID:g551534; PIDN:AAA21873.1, PID:g551535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 LISSSSSRPKKYICTYEGCDKAYNRPSLLEQHLRTHSNDRPYKCTVDDCDKAFFRKSHL
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16.7%; Score 372; DB 2; Length 393
Best Local Similarity 29.4%; Pred. No. 1.7e-15;
Matches 110; Conservative 57; Mismatches 163; Indels
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A,Cross-references: GDB:43744; OMIM:600860
A,Bostion: 13q12.3-13q13.1
G,Superfamily: transcription factor IIIA
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Best Local Similarity 29.0%;
Matches 89; Conservative 4
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                                                                                                                                                  383 SHFIAHHRI-HTGEKPYECSDCGKCFTKKSQL-RVHQKIHTGEKPNICAECGKAFTDRSN 440
                                                                                                                                                                                                                                                                                                     285 -LETEKLKVEEDEEDEEDS----LDEKRSDVRSDSMSAQRSI-----KSFTASLEGSKS 333
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A;Molecule type: mRNA
A;Residues: 1-651 <BEL>
A;Cross-references: 0B:M27878
C:Superfamily: zinc finger protein ZFP-36; LIM metal-binding repeat homology C;Keywords: tandem repeat
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16.7%; Score 373; DB 2; Length 651;
Best Local Similarity 27.4%; Pred. No. 2.6e-15;
Matches 128; Conservative 57; Mismatches 146; Indels 136; Gaps
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JN0533
JN0533
JNDGAT protein pMLZ-4 - mouse
C,Species: Mus musculus (house mouse)
                                                                                  NELVEHYNI FHDGNI PDD---
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Matches 128; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 265 VFSRNSYLAQHLIIHAGEKPYKCDECDKAFSQNSHLVQHHRIHTGEKPYKCDEGGKVFSQ 324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.7 EKTLITCKOCNKVPTRPSKLAQHKLKHHGGSPAYQCDHPGCFKNFQTWSVLQFHIKQSHPK 196
                                                                                                                                                                          197 LK---CPK--CGKGCVGKKGLSSHMLSHD-DSTMIKIWTCDYCDVGKPAKKNELVEHYNI 250
                                                                                                                                                                                        247 SRPFVCEHAGCGKTFAMKQSLTRHAVVHDPDKKKMKL.-----KVKKSREKRSLASHLS- 299
                                          PYKCTVDDCDKAFFRKSHLETHIVSHSEKKPFHCSV - - CGKGVNSRQHLKRH-EITH--- 107
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            32 CDKAYNRPSLLEQHLRTHSNDRPYKCTVDDCDKAFFRKSHLETHIVSHSEKKPFHCSVCG
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A;Residues: 1-428 <BEL>
A;Cross-references: GB:M27877
C;Superfamily: zinc finger protein ZFP-36; LIM metal-binding repeat
C;Superfamily: zinc finger protein ZFP-36; LIM metal-binding repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 428;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
16.3%; Score 364; DB 2; Length 428
Best Local Similarity 29.1%; Pred. No. 5.7e-15;
Matches 116; Conservative 50; Mismatches 155; Indels
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  KSISSL----ISSSSSR--
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Krueppal-related protein H-plk - human (Species: Homo sapiens (man) (Species: Homo sapiens (man) (Species: Homo sapiens (man) (Species: 28-Sep-1990 #sequence_revision 18-Nov-1992 #text_change 01-Dec-2000 (Spacession, N.; Shimotohno, K.; VanLeeuwen, D.; Cohen, M. M. (Shimotohno, K.; VanLeeuwen, D.; Cohen, M. M. (Shimotohno, R.; A101-4405, 1990 (Species of the provincal mRNAs down regulated in choriocarcinoma encode a zinc finger prolapsemence number: A35659; MuID:90318410; PMID:2115127 (Species of the provincal replainmary A; Molecule type: mRNA (Species: 1-427 ckAr) A; Molecule type: mRNA (Species: 1-427 ckAr) (Species: 1-427 ckAr) (Species: 1-427 ckAr) (Species: 1-427 ckAr) (Species: 1-427 ckAr) (Species: 1-427 ckAr) (Species: 1-427 ckAr) (Species: 1-427 ckAr) (Species: 1-427 ckAr) (Species: 1-427 ckAr) (Species: 1-427 ckAr) (Species: 1-427 ckAr) (Species: 1-427 ckAr) (Species: 1-427 ckAr) (Species: 1-427 ckAr) (Species: 1-427 ckAr) (Species: 1-427 ckAr) (Species: 1-427 ckAr) (Species: 1-427 ckAr) (Species: 1-427 ckAr) (Species: 1-427 ckAr) (Species: 1-427 ckAr) (Species: 1-427 ckAr) (Species: 1-427 ckAr) (Species: 1-427 ckAr) (Species: 1-427 ckAr) (Species: 1-427 ckAr) (Species: 1-427 ckAr) (Species: 1-427 ckAr) (Species: 1-427 ckAr) (Species: 1-427 ckAr) (Species: 1-427 ckAr) (Species: 1-427 ckAr) (Species: 1-427 ckAr) (Species: 1-427 ckAr) (Species: 1-427 ckAr) (Species: 1-427 ckAr) (Species: 1-427 ckAr) (Species: 1-427 ckAr) (Species: 1-427 ckAr) (Species: 1-427 ckAr) (Species: 1-427 ckAr) (Species: 1-427 ckAr) (Species: 1-427 ckAr) (Species: 1-427 ckAr) (Species: 1-427 ckAr) (Species: 1-427 ckAr) (Species: 1-427 ckAr) (Species: 1-427 ckAr) (Species: 1-427 ckAr) (Species: 1-427 ckAr) (Species: 1-427 ckAr) (Species: 1-427 ckAr) (Species: 1-427 ckAr) (Species: 1-427 ckAr) (Species: 1-427 ckAr) (Species: 1-427 ckAr) (Species: 1-427 ckAr) (Species: 1-427 ckAr) (Species: 1-427 ckAr) (Species: 1-427 ckAr) (Species: 1-427 ckAr) (Species: 1-427 ckAr) (Species: 1-427 ckAr) (Species: 1-427 ckAr) (Species: 1-427 ckAr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          191 KQSHPKLK---CPKCGKGCVGKK-GLSSHMLSHDDSTMIKIWTCDYCDVGKFAKKNELVE 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             359 HRTHTGEKPFSCSECGK-CYSKKSSLVHHQRTHTGEKPFSCSKCDKC----FASSSEL-- 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184
                                                                                                                                                                                                                                             finger protein (clone XlCOF7.1) - African clawed frog (fragment)
C.Species: Xenopus laevis (African clawed frog)
C.Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 01-Dec-2000
C.Accession: S06546
B.Nietfeld, W.; El-Baradi, T.; Mentzel, H.; Pieler, T.; Koester, M.; Poeting
J. Mol. Biol. 208 63-659, 1989
A.Title: Second-order repeats in Xenopus laevis finger proteins.
A.Reference number: S06532; MUID:90040698; PMID:2509712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        247 HYNIFHDGNIPDDLLKETEVKKLENLLDQGSKLNNLHELETEKLKVEEDEEDEEDEEDEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            307 RSDVRSDSMSAQRSIKSFTASLEGSKSVS-----KLISNSGKKINCPKNNCDRMFSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HLETHIVSHSEKKPFHCSVCGKGVNSRQHLKRHEITHT--KSFKCTFENCQEAFYKHQSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSLISSSSSRPKKYICTYEGCDKAYNRPSLLEQHLRTHSNDRPYKCTVDDCDKAFFRKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: mRNA
A;Residues: 1-615 <NNE>
C;Superfamily: zinc finger protein ZFP-36; LIM metal-binding repeat
C;Superfamily: zinc finger
C;Keywords: DNA binding; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                    419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 363.5; DB 2;
; Pred. No. 9.1e-15;
48; Mismatches 165;
383 SLTNHHAIHTGEKHFKC--NECGKLFRDNSYLVRHQRFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 27.6%;
Matches 119; Conservative 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              359 EYDLRRHLKWH 369
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246 ERRYECEECGRAFNRSSKLTEHKYIHTGEKLYKCEECGRAFNQSSTLTTHKRIHSGEKPY 305
                                                                                                                                                                                                                                                                                                                                                                           306 KCEE--CGKAFKQFSNUJDHKKIHTGEKPYKCEECGKAFNQLSNIJRHKVIH---TGEKP 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                     361 YKCGEC--GKAFNQSSALNTHKIIHTGENPHKCRESGKVFHL----SSKLSTCKKIHT 412
                                                                                                                                       80 SEKKPPHCSVCGKGVNSRQHLKRHEITHTKS--PKCTPFNCQEAFYKHQSL-RHHILSVH 136
                                                                                                                                                                                                                     137 EKTLICKOCNKVFTRPSKLAQHKLKH-------HGGSPAY 169
                                                                                                                                                                                                                                                                                                                                                  170 OCDHPGCFKNFQTWSVLQFH--IKQSHPKLKCPKCGKGCVGKKGLSSHMLSHDDSTMIKI 227
                                                                                                                                                                                                                                                                                                                                                                                                                            228 WTCDYCDVGKFAKKNELVEHYNIFHDGNIPDDLLKETEVKKLENLLDQGSKLNNLHELET 287
                                                                                                                20 SRPKKYICTYEGCDKAYNRPSLLEQHLRTHSNDRPYKCTVDDCDKAFRKSHLETHIVSH 79
C, Superfamily: zinc finger protein ZFP-36; LIM metal-binding repeat homology
                                    Query Match
16.1%; Score 359.5; DB 2; Length 427;
Best Local Similarity 32.0%; Pred. No. 1.1e-14;
Matches 99; Conservative 36; Mismatches 121; Indels 53; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            288 -EKL-KVEE 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   413 GEKLYKCEE 421
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